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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*

8: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*

9: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
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27
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Listing first 45 summaries
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                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988 DAT: *
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998 DAT: *
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49.176 Million cell updates/sec
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and is derived by analysis of the total score distribution. pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

SUMMARIES

10	9	8	7	6	ъ	4	ω	2	1	Result No.	
27	27	27	27	27	27	27	27	27	27	Score	
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match	dР
122	118	118	118	113	110	110	61	л	5	Query Match Length DB	
11	21	21	21	22	21	21	23	21	21	DB	
AAR04135	AAY51145	AAY51143	AAY59266	ABB71922	AAY51139	AAY59262	ABP07152	AAY51133	AAY59256	ID	
Anti-Leu 3a heavy	Murine derived pro	Murine derived pro	Antibody 4H5 H cha	Drosophila melanog	Murine derived pro	Antibody 4H5 H cha	Human ORFX protein	Murine CD4/CD34 re	Antibody 4H5 H cha	Description	

Human OREX ORE1469	AAB41705	21	249		26	45
Staphylococcus epi	ABP39000	23	233		26	44
Sa	AAE00803	22	223	σ	26	43
_	AAB07844	21	215	O,	26	42
idermidis	AAG83015	22	214	o,	26	41
. epidermidis	AAG82660	22	182	o	26	40
abidopsis tha	AAG55873	21	157	o	26	39
	AAG56331	21	146	01	26	38
S	AAU35109	22	139	٥١	26	37
=	AAY04862	20	127	O١	26	36 6
Arabidopsis thalia	AAG56333	21	122	96.3	26	ယ ပ
F	AAY04864	20	113	٥١	26	34
Human polypeptide	AA003006	22	102	٠	26	ω ω
Human glycosyl-pho	ABB04400	23	99	٠,	26	32
Human polypeptide	AA003560	22	97		26	31
MutB protein of th	ABB09640	23	990	\cdot	27	30
ylori	AAW98599	19	933		27	29
Drosophila melanog	ABB59200	22	778		27	28
Escherichia coli p	ABB52638	22	722	100.0	27	27
Drosophila melanog	ABB60600	22	616		27	26
Drosophila melanog	ABB63767	22	543		27	25
C. pneumoniae prot	AAY34756	20	507		27	24
reptococ	ABP29082	23	444		27	23
Human cancer assoc	AAB43940	21	399	100.0	27	22
B. cereus LeuDH pr	AAW40248	18	366		27	21
Putative P. abyssi	AAB96816	22	348		27	20
Pyrococcus horikos	AAY82330	21	348		27	19
Murine derived pro	AAY51142	21	305		27	18
derived	AAY51141	21	305		27	17
4H5 L	9	21	305	100.0	27	16
4H5 H	AAY59264	21	305		27	15
cus lac	ABB54572	23	303		27	14
Drosophila melanog	ABB68170	22	149		27	13
Anti-Leu 3a heavy	AAR04133	11	136	0	27	12
cret	AAB64639	22	131	100.0	27	11

ALIGNMENTS

663	PS PS	PT.	X R	PA	PR	PF	X P	X PN	XX SO	XX	X X	XX	X	×	AC	XX	ID	RESULT 1 AAY59256
The invention provides an antibody having affinity anti-human CD4 antibody 4H5 is used for the detecti	Claim 1; Page 14; 25pp; Japanese.	An antibody and the nucleic acid coding the antibod	WPI; 2000-091351/08.	(ASAH) ASAHI KASEI KOGYO KK.	26-MAY-1998; 98JP-0163034.	26-MAY-1998; 98JP-0163034.	07-DEC-1999.	JP11332563-A.	Mus sp.		CD4 antigen; anti-human; antibody; 4H5; drug; CDK; Complementarity determining region.	H Chain Variable region Coxi ita			AAY59256;		AAY59256 standard; peptide; 5 AA.	LT 1 9256

Claim 1; Page 14; 25pp; Japanese. An antibody and the nucleic acid coding the antibody -

The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and $\,$

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RESULT 2
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                                       Matches
                                                                                   Query Match
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                                                                                                                                                                             This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimmeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoinmune diseases. This sequence represents a murine derived complementarity determining region CDR-1 protein fragment which is used to illustrate the method of
                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 75; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Devices containing antibodies recognising CD4 or CD34 and their use for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ono M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-1998;
26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ASAH ) ASAHI MEDICAL CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ASAH ) ASAHI KASEI KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine CD4/CD34 recognizing antibody heavy chain CDR-1 region #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY51133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           application for drugs. It is highly safe in human dose. Sequences AAY59256-58 represent the complementarity determining region (CDR)-1, CDR-2 and CDR-3 fragments in the H chain variable region of the
                                                              Local Similarity
1 DYVIN 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 separation of CD4 or CD34 positive cells
                                                                                                                                                                        invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4H5 respectively.
                                                                                                                               U
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                                       Conservative
                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chain; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9940-JP02711. instut PCT privily
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98JP-0163023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morimoto I,
                                                         100.0%;
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                                                       Score 27; DB 21;
Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miyamura K;
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                                     Mismatches
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                                                                          Length 5;
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                                     Indels
                                0;
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                                                                                                                                                                                                                                            treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious
                                                                                                                                                                                 diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also
                                N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                reperfusion injury in various tissues and conditions resulting systemic cytokine damage.
                                                                                                                useful for treating burns, incisions, ulcers, for treating osteoporosis bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis,
             at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Tab in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID 14286; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000; 2000US-206132P
29-AUG-2000; 2000US-228716P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAY-2001; 2001WO-US10836.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ORFX protein sequence SEQ ID NO:14286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP07152 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUN-2002 (first entry)
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23 DYVIN 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC,
                                                                       26-MAY-1998;
         WO9961629-A1
                                                               25-MAY-1998;
                           02-DEC-1999
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                                                The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the H chain variable region of the antibody 4H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                   100.0%; Score 27; DB 23; Length 61; ilarity 100.0%; Pred. No. 35; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                              An antibody and the nucleic acid coding the antibody
                                                                                                                                                                                                   CD4 antigen; anti-human; antibody; 4H5; drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                Antibody 4H5 H chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine derived protein fragment #1.
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                                                                                                                          AAY59262 standard; protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 15; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                  (ASAH ) ASAHI KASEI KOGYO KK
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                                                                                                                                                                 17-APR-2000 (first entry)
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Matches 5; Conservative
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N-PSDB; AAZ58661.
                Query Match
Best Local Similarity
5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 AA;
      61 AA;
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24 DYVIN 28
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                                                            1 DYVIN 5
                                                                                                                                                                                                                                                                                26-MAY-1998;
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                                                                                                                                               AAY59262;
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         Sednence
                                                                                                                                                                                                                           Mus sp.
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                                                                                                            RESULT 4
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This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34 positive cells, which is useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                    Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 27; DB 21; Length 110; 100.0%; Pred. No. 69;
9940-JP02711. wint PUT punt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 22; Page 78; 111pp; Japanese
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                                                                                                                                                                                    (ASAH ) ASAHI KASEI KOGYO KK
                                                                                                                                                                                                            (ASAH ) ASAHI MEDICAL CO LTD.
                                                                                              98JP-0159957
                                                                                                                             98JP-0163023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PEKE ) PE CORP NY.
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les 5; Conserv
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics and pharmaceutical drugs. The invention signalcoloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16177-ABL30511), appressed DNA conservances (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                            0;
                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                         (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents a H chain fragment of the antibody 4H5.
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                       Disclosure; SEQ ID NO 42558; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                             Length 113;
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                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 27; DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD4 antigen; anti-human; antibody; 4H5; drug.
                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY59266 standard; protein; 118 AA.
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   2001-656860/75.
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Best Local Similarity
Matches 5; Conserv
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N-PSDB; AAZ58689.
                                                                                                                                                                                                                                                                                                                       113 AA;
                 N-PSDB; ABL16025
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                                                                              Interactions
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| 54 DYVIN 58
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Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoletic undifferentiated cells, elimination of detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Soka T, Morimoto I, Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 94-95; 111pp; Japanese.
                          AAY51143 standard; Protein; 118 AA.
                                                                                                                  Murine derived protein fragment #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY51145 standard; Protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                      (ASAH ) ASAHI KASEI KOGYO KK. (ASAH ) ASAHI MEDICAL CO LTD.
                                                                                                                                                                                                                                                                                                                                            98JP-0163023.
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                                                                                    31-MAR-2000 (first entry)
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es 5; Conserv
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RESULT
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Best Local Similarity 100. Matches 5; Conservative

Murine derived protein fragment #7.

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This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the lymphocytes from cells and the production of medicinal detection of leukemic cells and the production of medicinal compositions for the treatment of HV infection and autoimmune diseases. Compositions to the treatment of HV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
    Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                   Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells \, ^{-}
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                                                                                                                                                                                                                                                                        Soka T, Morimoto I, Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 96-97; 111pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR04135 standard; protein; 122 AA.
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                                                                                                                                                           99WO-JP02711.
                                                                                                                                                                                                                                  (ASAH ) ASAHI KASEI KOGYO KK.
                                                                                                                                                                                                                                               ASAH ) ASAHI MEDICAL CO LTD.
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31 DYVIN 35
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                                                                                  Mus sp.
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The invention relates to the isolation of genes AAF32757-F32803 encoding the human secreted proteins AAB64549-B64594. The sequence is a search result from a BLASTX homology search. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by for protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                         Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be used to form chimeric mouse-variable, human-constant region Abs suggested as being useful as a vaccine to HIV.
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                                                                                                                                                                                                                                               100.0%; Score 27; DB 11; Length 122; 100.0%; Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein BLAST search protein SEQ ID NO: 149.
                                                                                           New chimeric variants of murine antibody anti-leucine -contg. human antibody regions, and DNA encoding sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                            AAB64639 standard; Protein; 131 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2000; 2000WO-US14934.
                                                                                                                                          Claim 5; Fig 5; 12pp; English.
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    (BECT ) BECTON DICKINSON CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-032312/04.
                                                                                                                                                                                                                                                                       Local Similarity
nes 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ROSE/) ROSEN C A.
                                                           WPI; 1990-126329/17
                                                                                                                                                                                                                                 122 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200077197-A1.
                                    Oi VT;
                                                                          N-PSDB; AAQ04042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                             35 DYVIN 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-DEC-2000.
                                                                                                                                                                                                                                                                                                                   1 DYVIN 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAR-2001
                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB64639;
                                      Hinton R,
                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                      AAB64639
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and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound and (f) infectious diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used to form chimeric mouse-variable, human-constant region Abs suggested as being useful as a vaccine to HIV.
                                                                                                                                                                                                          ó
                                                                                                                                                                      100.0%; Score 27; DB 22; Length 131; 100.0%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                              Anti-Leu 3a heavy chain variable region gene product, 316 Vh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 27; DB 11; Length 136; 100.0%; Pred. No. 88; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New chimeric variants of murine antibody anti-leucine -contg. human antibody regions, and DNA encoding sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Variants of murine monoclonal anti-CD4 antibody,
                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                     AAR04133 standard; protein; 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        HIV; AIDS; anti-Leu3A; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 3; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89EP-0N10415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BECT ) BECTON DICKINSON CO.
                                                                                                                                                                                                                                                                                                                                                      06-SEP-1990 (first entry)
                                                                                                                                                                                           5; Conservative
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                                                                                                                                                                               Local Similarity
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N-PSDB; AAQ04040.
                                                                                                                                         Sequence 131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oi VT;
                                                                                                                                                                                                                                    66 DYVIN 70
                                                                                                                                                                                                                    1 DYVIN 5
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-0CT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-APR-1990.
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49 DYVIN 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP365209-A.
                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hinton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                               JLT 12
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is cell-neal in developmental biology and in elucidating cell signalling and insecticides, theractions in higher eukaryotes for the development of discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                        Drosophila, developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, SEO ID NO 31302; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 27; DB 22; Length 149; 100.0%; Pred. No. 98; tive 0; Mismatches 0; Indels (
                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 31302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myers EW;
ABB68170 standard; Protein; 149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB54572 standard; Protein; 303 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
es 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 AA;
                                                                                                                                                                                                                                                                                                                                                                                       WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABL12273
                                                                                                                            26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001.
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THE SECOND SECON
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FRESULT 13 ABB68170

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The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yourt and cheese.

Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides an antibody having affinity to CD4 antigen. The
                                                                                                                                                                                  nucleotide sequence useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 27; DB 23; Length 303; 100.0%; Pred. No. 2.2e+02; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An antibody and the nucleic acid coding the antibody
                                                                                                                          Bolotine A, Sorokine A, Renault P, Ehrlich SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD4 antigen; anti-human; antibody; 4H5; drug.
                                                                                                                                                                                                                                    Claim 6; SEQ ID No 1274; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 16-17; 25pp; Japanese
                                                                                                (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY59264 standard; protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody 4H5 H chain sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98JP-0163034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98JP-0163034.
                                                                                                                                                                                                         lactis and related species -
                                 11-APR-2000; 2000FR-0004630.
                                                                   11-APR-2000; 2000FR-0004630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-091351/08.
                                                                                                                                                            WPI; 2002-043418/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ58663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 DYVIN 213
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           12-OCT-2001
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AAY59264
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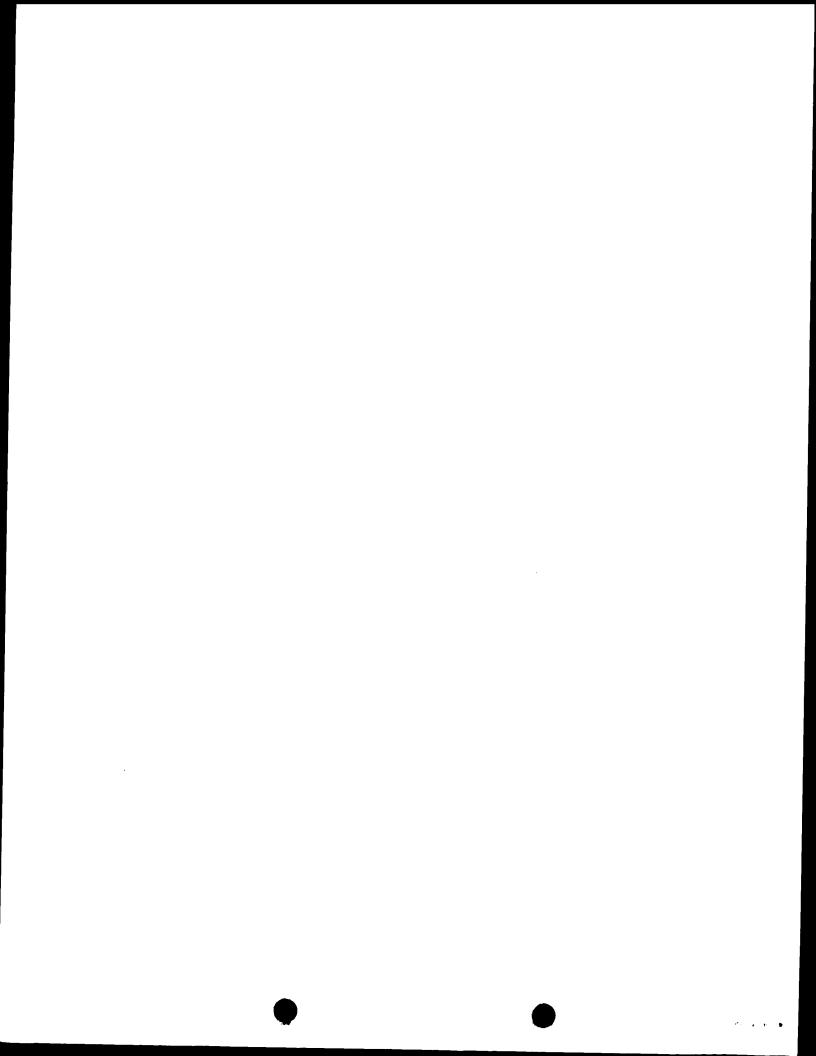
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anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the H chain sequence of the antibody 4H5.
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                                                                                                      Length 305,
                                                                                                                                         0; Indels
                                                                                                      100.0%; Score 27; DB 21;
100.0%; Pred. No. 2.2e+02;
tive 0; Mismatches 0;
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Sequence 3983, Ap Sequence 9, Appli Sequence 4937, Ap Sequence 45, Appli Sequence 6, Appli Sequence 6, Appli Sequence 11, Appli
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3845, Ap
1, Appli
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atent No. 5204096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                   February 14, 2003, 11:13:07; Search time 4.51613 Seconds (without alignments) 32.575 Million cell updates/sec
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Sequence 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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'CGDZ_G/Ptodata1/jaa/5A_COMB.pep:*
'CGDZ_G/Ptodata1/jaa/5B_COMB.pep:*
'CGDZ_G/Ptodata1/jaa/6A_COMB.pep:*
'CGDZ_G/Ptodata1/jaa/6B_COMB.pep:*
'CGDZ_G/Ptodata1/jaa/6B_COMB.pep:*
'CGDZ_G/Ptodata1/jaa/PCTUS_COMB.pep:*
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-627-376-7

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US-09-134-001C-845-6

US-08-104-001C-845-6

US-08-80-66-888A-3

US-08-35-844-1

PCT-US9-16126-1

US-09-13-750A-35-6

US-09-113-750A-35-6

US-08-13-750A-35-6

US-08-13-581-4

US-08-913-581-4

US-08-913-581-4

US-08-913-581-4

US-08-913-581-4

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US-09-134-001C-4937
US-08-423-399B-35
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US-08-530-950-11
US-08-888-429A-11
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US-09-594-185-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262574 seqs, 29422922 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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27
1 DYVIN 5
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                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
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11, Appl 12, Appl 17, Appl 17, Appl 12, Appl 12, Appl 17, Appl 10, Appl 20, Appl 20, Appl 118, Appl 3182, Appl 3182, Appl 3182, Appl 3182, Appl 3182, Appl 3182, Appl		THE PREPARATION	Gaps 0;	
Sequence 11 Sequence 13 Sequence 13 Sequence 13 Sequence 13 Sequence 13 Sequence 15 Sequence 15 Sequence 15 Sequence 15 Sequence 23 Sequence 24 Sequence 24 Sequen		NUCLEOTIDE	Length 366; Indels 0;	
393 4 US-09-149-879-11 400 1 US-08-530-950-12 400 2 US-08-878-989-3 400 4 US-09-878-989-17 400 4 US-09-272-796-3 400 4 US-09-272-796-3 400 4 US-09-272-796-3 400 4 US-09-272-796-3 400 4 US-09-134-001C-5006 522 4 US-08-961-083-12 736 4 US-09-562-737-98 1040 4 US-08-961-083-118 2544 2 US-09-134-001C-3182 253 4 US-09-134-001C-3182 254 2 US-09-134-001C-5053 362 4 US-09-134-001C-5053	ALIGNMENTS	on US/08804699 ', TANJA MARIA-REGINA E ENZYME WITH LEUDH ACTIVITY, E ENZYME WITH LEUDH ACTIVITY, E SEQUENCE CODING THEREFOR AND SIS. 2 RESS: SSUBRY, MADISON & SUTRO, L.L.P. WAYORK AVENUE, N.W. NA TO COMPATIBLE C COMPATIBLE C COMPATIBLE C COMPATIBLE C COMPATIBLE FFORM: NA NA NA NA NA NA NA NA NA N	100.0%; Score 27; DB 2; Le 100.0%; Pred. No.1.1e+02; vative 0; Mismatches 0;	
00000000000000000000000000000000000000		99-2 2, Application 5, S854035 INFORMATION: ANT: STOYAN, ANT: KULA, MA OF INVENTION: O	imilarity ; Conser	N 5 - 289
22422222222222222222222222222222222222		Sequence 2, Application US, Sequence 2, Application US, Sequence 2, Application US, Sequence 2, Application US, Sequence 2, Application SEGUERAN: TAN APPLICANT: STULA, MARIA TITLE OF INVENTION: SETTLE OF INVENTION: OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSES. ADDRESSES. ADDRESSES. ADDRESSES. ADDRESSES. STREET: U.S.A. STREET: U.S.A. STREET: U.S.A. STREET: U.S.A. STREET: D.C. COUNTRY: U.S.A. STREET: D.C. COMPUTER READABLE FORM: MEDIUM TYPE: IBM PC CONCOMPUTER READABLE FORM: MEDIUM TYPE: IBM PC CONCOMPUTER READABLE FORM: MEDIUM TYPE: DATE OF SOFTWARE: PATLONION AND STREET STREET ON UNMBER: FILING DATE: 202-861-TELEPHONE: 202-861-TELEFTAX: 202-822-09] TELEPHONE: 305-822-09] TELEFAX: 202-822-09] TONDORDICE CHARACTERISTIC LENGTH: 366 amino acid TYPE: amino acid	ttch sals	1 DYVIN 285 DYVIN
222 E E E E E E E E E E E E E E E E E E		RESULT 1 US-08-804-[Sequence Patent N APPLIC APPLICA	Query Ma Best Loc Matches	Qy Db 2:
		K D A R A R A R A R A R A R A R A R A R A		

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PatentIn Release #1.0, Version #1.30
                                                        TYPE: PRT ORGANISM: Staphylococcus epidermidis
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225 Franklin Street
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; Patent No. 5942431
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 3, Application US/08606888A ; Patent No. 5766913
                                                                                                                                                                           4; Conservative
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3845
LENGTH: 233
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Matches 4; Conservative
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                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserva
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STREET: 220
-wv. Boston
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219 DYIIN 223
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US-08-606-888A-3
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LENGTH: 288
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Patent No. 6380370
GENERL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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| Sequence 4.2 Application US/09247373B
| Patent No. 6168954
| GENERAL INFORMATION:
| APPLICANT: MCGONIGLE, BRIAN
| APPLICANT: MCGONIGLE, BRIAN
| TITLE OF INVENTION: SOUREAL GLUTATHIONE-S-TRANSFERASE ENZYMES
| FILE REFERENCE: CL-1108-A
| CURRENT APPLICATION NUMBER: US/09/247,373B
| PRIOR FILING DATE: 1999-02-10
| PRIOR FILING DATE: 1999-06-10
| PRIOR FILING DATE: 1997-09-05
| NUMBER OF SEQ ID NOS: 56
| SOUTHARRE: MICROSOFT Office 97
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                                  Sequence 7, Application US/09627376
Patent No. 6342385
GENERAL INFORMATION:
APPLICANT: 01, Fengxia Caufield, Page Chen, Ping TITLE OF INVENTION: MTPACIN I BIOSYNTHESIS GENES AND PROTEINS TILE REFERENT APPLICATION NUMBER: US/09/627,376
CURRENT APPLICATION NUMBER: US/09/627,376
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 27; DB 4; Length 990; 100.0%; Pred. No. 3.3e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.3%; Score 26; DB 4; Length 215;
80.0%; Pred. No. 1e+02;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                          ORGANISM: Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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atches 5; Conserv
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US-09-134-001C-3845
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  RESULT 2
US-09-627-376-7
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                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                   Query Match
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Gaps
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APPLICANT: HARUM, TAABSHI
APPLICANT: HARUM, TAKADA

APPLICANT: HALUM, TAKADA

APPLICANT: HALL

APPLICAN
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APPLICANT: Lin, Shuen-Fuh
APPLICANT: Chiou, Chien-Ming
APPLICANT: Chiou, Chien-Ming
APPLICANT: Chiou, Chien-Hiang
TITLE OF INVENTION: CLONING, EXPRESSION AND NUCLEOTIDE
TITLE OF INVENTION: SEQUENCE OF A AKALINE GENE FROM PSEUDOMONAS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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                             Length 233;
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80.0%; Pred. No. 1.4e+02;
Live 1; Mismatches 0; Indels
96.3%; Score 26; DB 4; Length 233
80.0%; Pred. No. 1.1e+02;
tive 1; Mismatches 0; Indels
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1 DYVIN 5
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                                                     NAME/KEY:
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                                                                                                                                                            US-08-355-844-1
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                   FEATURE:
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96.3%; Score 26; DB 1; Length 338

Best Local Similarity 80.0%; Pred. No. 1.7e+02;

Matches 4; Conservative 1; Mismatches 0; Indels
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| Sequence | Application US/08355844 |
| Patent No. 5940307 |
| GENERAL INFORMATION: |
| APPLICANT: Escapledy, Ference |
| APPLICANT: Iserovich, Pavel |
| APPLICANT: Li, Jun |
| APPLICANT: Li, Secondary |
| TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN |
| TITLE OF INVENTION: STRUCTURE |
| NUMBER OF SEQUENCES: 3 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond |
| STREET: 30 Rockefeller Plaza |
| CITY: New York |
| CORRESPONDENCE |
| CITY: New York |
| 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A29927-50/29910
                                                                                                                                                                                                                                                06840/003001
                      APPLICATION NUMBER: US/08/606,888A FILING DATE: 26-FEB-1996 CLASSIFICATION: 435
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FILING DATE: 14-DEC-1994
CLASSIFICATION: 436
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: TAIG, Henry Y.S.
REGISTRATION NUMBER: 29,705
REFERENCE/DOCKET NUMBER: A299
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-286
TELEPHONE: 212-765-2519
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                                                                                                                                                                                                                                                                                                                                                    TELEFAX: ...,
TELER: 200154
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 338 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 066
TELECAMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPRAX: 617/542-8906
                                                                                                                                     ATTORNAL TSAO, ROCKY Y.
REGISTRATION NUMBER: 34,053
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
CURRENT APPLICATION DATA:
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10112-0228
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241 DYVVN 245
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80.0%; Pred. No. 1.7e+02;
tive 1; Mismatches 0; Indels
                                                                                                                          96.3%; Score 26; DB 2; Length 340;
80.0%; Pred. No. 1.7e+02;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fischbarg, Jorge
APPLICANT: Czegledy, Ferenc
APPLICANT: Iserovich, Pavel
APPLICANT: Li, Jun
APPLICANT: Li, Jun
APPLICANT: Cheung, Min
TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN
TITLE OF INVENTION: STRUCTURE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/16126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A29927-50/29910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , LUCATION: 1..340
; OTHER INFORMATION: OmpF porin protein
PCT-US95-16126-1
                                                        LOCATION: 1.340
OTHER INFORMATION: OmpF porin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/355,844
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application PC/TUS9516126
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Tang, Henry Y.S.
REGISTRATION NUMBER: 29,705
REFRENCE/DOCKET NUMBER: A299
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2586
TELEPHONE: 212-765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO: 1:
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 80.0 Matches 4; Conservative
                                                                                                                 Query Match
Best Local Similarity 80.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide ORIGINAL SOURCE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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                                      Peptide
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ZIP: 10112-0228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
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ORIGINAL SOURCE:
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          COUNTRY:
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TOPOLOGY:
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US-08-403-866-7
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                                                                                                                                                              APPLICANT: AIYAR, NAMBI V.
APPLICANT: AIYAR, NAMBI V.
APPLICANT: DISA, JYOTI
TITLE OF INVENTION: BECRER:BOVINE CALCITONIN RECEPTOR-LIKE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.3%; Score 26; DB 3; Length 462;
80.0%; Pred. No. 2.4e+02;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL TREORMATION:
GENERAL TREORMATION:
GENERAL BAVID E. Junker and Mark D. Cochran
TITLE OF INVENTION: Recombinant Raccoonpox virus
TUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/238,796
FILING DATE: 28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 35, Application US/09113750A Patent No. 6294176
                                                                                                                 Sequence 2, Application US/09238796
Patent No. 6074845
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFRENCE/DOCKET NUMBER: GP-7C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                     ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 80.0%;
"Thes 4; Conservative
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MOLECULE TYPE: protein
09-238-796-2
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                                                                                                                                                                                                                                                                                                                                       USA
                                 312 DYIIN 316
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367 DYIIN 371
1 DYVIN 5
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                                                                                                   US-09-238-796-2
                                                                                                                                                                                                                                                                                                         CITY: V
STATE:
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                                                                                 RESULT 9
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Gaps
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APPLICANT: Ehrlich, Stanislav
APPLICANT: Ehrlich, Stanislav
APPLICANT: Godon, Jean-Jacques
APPLICANT: Godon, Jean-Jacques
APPLICANT: Remault, Pierre
TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
TITLE OF INVENTION: Synthase from Lactococcus and its applications
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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80.0%; Pred. No. 2.8e+02;
tive 1; Mismatches 0; Indels
COMPUTER READABLE FORM:
MEDULUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/403,866
                                                                                                                                         APPLICATION NUMBER: US/09/113,750A
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30, 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 7, Application US/08403866
; Patent No. 5643779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 2074, TELECOMMUNICATION INFORMATION: TELEFAX: (716) 263-1487 TELEX: 978450 (WUT) INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LEWGTH: 575 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 557
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)262-0400
                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-113-750A-35
                                                                                                                                                                                                                                                                                                                                                           TELEX: 422523
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 525 amino acids
                                                                                                                                                                                                                                                                                                                                          (212)664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.37
Best Local Similarity 80.07
Matches 4; Conservative
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                                                                                                                                                               FILING DATE:
CLASSIFICATION: 424
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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GENERAL INFORMATION:
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Pred. No. 4.4e+02;
1; Mismatches 0; Indels
                                                                                                       Score 26; DB 1; Length 575;
Pred. No. 3.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Hodgson, John
APPLICANT: Lawlor, Elizabeth
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5756329el tRNA Synthetase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/785,052
FILING DATE: 17-JAN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 9601096.2
FILING DATE: 19-JAN-1996
APPLICATION NUMBER: 9615845.6
FILING DATE: 27-JUL-1996
APPLICATION NUMBER: 9615845.6
FILING DATE: 27-JUL-1996
APPLICATION NUMBER: 9615845.6
FILING DATE: 27-JUL-1996
APPLICATION NUMBER: 381891
REGISTRATION NUMBER: AMBRITIN:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
יאנים במנסכסכנט lactis subsp. lactis individual isolaTE: ILVB
US-08-403-866-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: P31354-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 4, Application US/08913581
; Patent No. 5948657
                                                                                                                                                                                                                                                                                                  US-08-785-052-4; Sequence 4, Application US/08785052; Patent No. 5756329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.3%;
80.0%;
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                                                                                                             96.3%;
80.0%;
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amino acid
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Best Local Similarity 80.0°
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                                                                                             Ouery Match
Best Local Similarity 80.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-08-785-052-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             607 DYVVN 611
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278 DYIIN 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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TITLE OF INVENTION: Biosynthetic Process For The Preparation
TITLE OF INVENTION: Of Chemical Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match

96.3%; Score 26; DB 2; Length 800.

Best Local Similarity 80.0%; Pred. No. 4.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels
                                No. 5948657el tRNA Synthetase
                                                                                                                                                                                                                                                                                       SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/913,581
                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G tz, Friedrich
Schnell, No. 5837485bert
Augustin, Johannes
Engelke, Germar
Rosenstein, Ralf
Kaletta, Cortina
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 007/00/0022
APPLICATION NUMBER: 9601096.2
FILING DATE: 19-JAN-1996
APPLICATION NUMBER: 9615845.6
FILING DATE: 27-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/08392625; Patent No. 5837485; GENERAL INFORMATION: APPLICANT: Entian, Karl-Dieter
                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/785,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
APPLICANT: Hodgson, John
APPLICANT: Lavlor, Blizabeth
TITLE OF INVENTION: No. 59488
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wieland, Bernd
Kupke, Thomas
Jung, G nther
                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 800 amino acids
TYPE: amino acid
                                                                                                                                                   ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Dieter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cora
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                                                                                                                                                                                                                                     Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-913-581-4
                                                                                                                                     King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      607 DYVVN 611
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APPLICANT:
APPLICANT:
                                                                                                                                         CITY: King
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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US-08-392-625-20
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26; DB 2; Length 990, Pred, No. 5.6e+02;
                                                                                                                                         COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,625
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      0652.0980002
                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,791
FILING DATE: 30-ARR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G tz, Friedrich
Schnell, No. 5843709bert
Augustin, Johannes
Engelke, Germar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/08466961A Patent No. 5843709 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Entian, Karl-Dieter
                                                                                                                                                                                                                                                                                                                                                                               NAME: ESMOND, ROBERT W. 83 REGISTRATION NUMBER: 32,893 REFERENCE/DOCKET NUMBER: 06 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2640
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 96.3%;
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosenstein, Ralf
APPLICANT: Kaletta, Cortina
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Kupke, Thomas
Jung, G nther
Kellner, Roland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 990 amino acids
TYPE: amino acid
TOPOLOGY: linear
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CORRESPONDENCE ADDRESS:
                                                                                                        'RY: U.S.A.
20005
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RY: U.S.A.
20005
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                                                                                           STATE: D.C.
                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||:||
248 DYIIN 252
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                            COUNTRY:
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APPLICANT:
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COUNTRY:
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SOFTWARE: Perbos/Ms-Dos
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PELICATION NUMBER: US/08/466,961A
FILING DATE: 06-UN-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/784,234
FILING DATE: 30-ARR-1992
PRIOR APPLICATION NUMBER: US 07/784,234
FILING DATE: 31-0CT-1991
ATTORNEY AGRETIAND NUMBER: 3.893
PRIOR APPLICATION NUMBER: 3.993
PRIOR APPLICATION NUMBER: 3.993
PRIOR APPLICATIO
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February 14, 2003, 11:15:53; Search time 2.90323 Seconds (without alignments) 44.001 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                             140259 seqs, 25548876 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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27
                                                                                                                                                                                                                                             1 DYVIN 5
                                                                                                                                                                                                     Title:
Perfect score:
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Published_Applications_AA:*

1: /cgnz_6/ptodata/1/pubpaa/PCN_REM_DUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCN_REM_DUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/NCN_REM_DUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USOG_NUBM_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USOG_NUBM_POP:*

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12: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

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14: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					SUMMARIES		
Result No.	Score	% Query Match	% Query Match Length DB	DB	di.	Description	
-	27	100.0		10	US-09-925-301-1385	Sequence 1385, Ap	
7	27	100.0		12	US-10-047-676A-7	Sequence 7, Appli	
3	26	96.3	139	10	US-09-815-242-10702	Sequence 10702, A	
4	26	96.3	343	10	US-09-815-242-5705	Sequence 5705, Ap	
2	26	96.3	354	10	US-09-815-242-12464	Sequence 12464, A	
9	26	96.3	658	10	US-09-815-242-10947	Sequence 10947, A	
7	26	96.3	792	10	US-09-815-242-5411	Sequence 5411, Ap	
89	26	96.3	800	10	US-09-815-242-12366	Seguence 12366, A	
6	26	96.3	800	10	US-09-815-242-12985	Sequence 12985, A	
10	26	96.3	801	10	US-09-815-242-4879	Sequence 4879, Ap	
11	26	96.3		10	US-09-815-242-11522	Seguence 11522, A	
12	26	96.3	1349	10	US-09-815-242-5898	Sequence 5898, Ap	
13	26	96.3		10	US-09-815-242-13137	Sequence 13137, A	
14	25	95.6	118	10	US-09-905-243-70	Sequence 70, Appl	
15	25	95.6		10	US-09-755-665-38	Sequence 38, Appl	
16	25	97.6		10	US-09-815-242-13118	Sequence 13118, A	
17	25	97.6	306	10	US-09-815-242-5895	Sequence 5895, Ap	
18	25	97.6		10	US-09-755-665-64	Sequence 64, Appl	
19	25	95.6	387	12	US-10-033-078-6	Sequence 6, Appli	

Sequence 11, Appl Sequence 11, Appl Sequence 13, Appl Sequence 12188, A Sequence 12188, A Sequence 1284, Appl Sequence 120, Appl Sequence 2, Appl Sequence 2, Appl Sequence 120, Appl Sequence 120, Appl Sequence 120, Appl Sequence 12543, A Sequence 12543, A Sequence 12543, A Sequence 12543, A Sequence 11770, A Sequence 11770, A Sequence 13845, A Sequence 13845, A Sequence 13845, A Sequence 13845, A Sequence 13643, A Sequence 13643, A Sequence 13643, A Sequence 13643, A	'n
0 US-09-755-665-36 0 US-09-761-569-11 0 US-09-761-569-12 0 US-09-761-569-12 0 US-09-815-242-5329 0 US-09-815-242-12188 0 US-09-912-020-381 0 US-09-912-020-381 0 US-09-912-020-381 0 US-09-912-020-381 0 US-09-912-020-381 0 US-09-912-020-381 0 US-09-912-020-381 0 US-09-815-242-1364 0 US-09-815-242-11770 0 US-09-815-242-11770 0 US-09-815-242-11770 0 US-09-815-242-11770 0 US-09-815-242-113845 0 US-09-815-242-13845 0 US-09-815-242-13845 0 US-09-815-242-13845 0 US-09-815-242-13561 0 US-09-815-242-13561 0 US-09-815-242-13561 0 US-09-815-242-13661 0 US-09-815-242-13661	US-09-978-756
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ALIGNMENTS

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Gaps
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                                                              GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEC ID NO 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 27; DB 10; Length 399; Best Local Similarity 100.0%; Pred. No. 70; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Qi, Fengxia
APPLICANT: Caufield, Page W.
APPLICANT: Chen, Ping W.
TITLE OF INVENTION: MUTAGIN I BIOSYNTHESIS GENES AND PROTEINS
FILE REFERENCE: UAB-17403/22
CURRENT APPLICATION NUMBER: US/10/047,676A
                      Sequence 1385, Application US/09925301
; Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 7, Application US/10047676A; Patent No. US20020123105A1
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-925-301-1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 DYVIN 308
US-09-925-301-1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DYVIN 5
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                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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TYPE: PRT ORGANISM: Staphylococcus aureus
                                                       Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                                                                                        APPLICANT: Trawick, John D. APPLICANT: Carr, Grant J. APPLICANT: Yamamoto, Robert
                              APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 80.0
Matches 4; Conservative
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                                                                                APPLICANT
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0
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100.0%; Score 27; DB 12; Length 990;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.3%; Score 26; DB 10; Length 139; 80.0%; Pred. No. 40; 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GASTLOCK, AUGUST,
APPLICANT: GASTLOCK, AUGUST,
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Kamamocto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE OF INVENTION: Prokaryotes
FILE OF INVENTION: Prokaryotes
FILE OF INVENTION: PROKARYOTES
CURRENT APPLICANTON NUMBER: US/09/815,242
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10702
LENGTH: 139
CURRENT FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 09/627,376
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 equence 10702, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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US-09-815-242-5705
$\$, Sequence 5705, Application US/09815242
; Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10702
                                                                                                                                                                   TYPE: PRT ORGANISM: Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                         185 DYVIN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SULT 3
09-815-242-10702
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17 DYVVN 21
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                                                                                                                      SEQ ID NO 7
LENGTH: 990
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Gaps
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APPLICANT: TIGALICA, JOHN D.
APPLICANT: Vamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: PROKATYOLES
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-102-16
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5705
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 12464, Application US/09815242; Patent No. US20020061569A1
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Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                        96.3%; Score 26; DB 10; Length 354; 80.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-0216
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SOFTWARE: FastSEQ for Windows Version 4.0
                           PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12464
LENGTH: 354
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            PRIOR APPLICATION NUMBER: 60/257,931
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                                                                                                                                                                                                 TYPE: PRT ; ORGANISM: Staphylococcus aureus US-09-815-242-12464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                            US-09-815-242-10947
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US-09-815-242-5411
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213 DYVVN 217
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US-09-815-242-10947
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Pred. No. 2.3e+02;
1; Mismatches 0; Indels
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APPLICANT: 2yskind, Judith W.
APPLICANT: 2yskind, Judith W.
APPLICANT: wall, Daniel
APPLICANT: Travick, John D.
APPLICANT: Tranier, John D.
APPLICANT: Tamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FULLARIA APPLICANTON NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                     APPLICANT: TIMELE, Grant J.
APPLICANT: Cart. Grant J.
APPLICANT: Vamamoto, Robert T.
APPLICANT: Xu, H. Howard Lication of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/19,078
PRIOR FILING DATE: 2000-05-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTERQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
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; Sequence 12366, Application US/09815242
; Patent No. US20020061569A1
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PRIOR APPLICATION NUMBER: 60/253,625
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80.0%;
                            Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
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Matches 4; Conserva
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SOFTWARE: Fasts
SEQ ID NO 5411
                                                                                        APPLICANT:
APPLICANT:
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                                  APPLICANT:
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80.0%; Pred. No. 2.4e+02;
Live 1; Mismatches 0; Indels
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80.0%; Pred. No. 2.4e+02;
Live 1; Mismatches 0; Indels
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Sequence 12985, Application US/09815242

GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari L.
APPLICANT: Apslication Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Wall, Wander C.
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-28
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,938
PRIOR APPLICATION NUMBER: 60/253,938
PRIOR PLICATION NUMBER: 60/269,308
PRIOR PLICATION NUMBER: 60/269,308
PRIOR PLICATION NUMBER: 60/269,308
PRIOR PLICATION NUMBER: 60/205, BRIOR PLICATION NUMBER: 60/269,308
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PRIOR PLICATION NUMBER: 60/205, BRIOR PLICATION NUMBER: 60/269,308
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; PRIOR FILING DATE: 2000-11-27; PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22; PRIOR PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16; NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 12366
; LENGTH: 800
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12985
LENGTH: 800
                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Staphylococcus aureus US-09-815-242-12366
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; ORGANISM: Staphylococcus aureus
US-09-815-242-12985
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Best Local Similarity 80.00
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Best Local Similarity 80.vv
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RESULT 10 US-09-815-242-4879

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                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,737
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-10-2-2
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TITLE OF INVENTION: Identification of Essential Genes in
FILLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4879
Sequence 4879, Application US/09815242
Patent No. US20020061569A1
PERERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11522, Application US/09815242 Patent No. US20020061569A1
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Enterococcus faecalis US-09-815-242-4879
                                                                                                                                                                                                                                       Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                        Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                             Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                               Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
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US-09-815-242-13137
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96.3%; Score 26; DB 10; Length 1349;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 96.3%; Score 26; DB 10; Length 1167; Best Local Similarity 80.0%; Pred. No. 3.5e+02; Matches 4; Conservative 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: 2918-0, MAIL L.
APPLICANT: 2918-0, Judith W.
APPLICANT: 4011, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yau, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential
FILE REFERENCE: ELITRA.011A
CURRENT APLICATION NUMBER: 05/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5898
                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-815-242-5898; sequence 5898, Application US/09815242; patent No. US20020061569A1
   PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; CRGANISM: Staphylococcus aureus
US-09-815-242-5898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Helicobacter pylori
US-09-815-242-11522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1101 DYVVN 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 DYVVN 399
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                                                                                                                                                                                                                                                     SEQ ID NO 11522
LENGTH: 1167
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RESULT 13

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Taylor, Alexander H
APPLICANT: Taylor, Alexander H
TITLE OF INVENTION: Monoclonal Antibodies with Reduced
TITLE OF INVENTION: Immunogenicity
FILE REFERENCE: P50770
CURRENT APPLICATION NUMBER: US/09/905,243
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR APPLICATION NUMBER: 1999-04-28
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                         APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: ELL'IKABLEH.

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-28

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-25

PRIOR FILING DATE: 2000-12-25

PRIOR FILING DATE: 2000-12-27

PRIOR FILING DATE: 2001-12-27

PRIOR FILING DATE: 2001-12-27

PRIOR FILING DATE: 2001-12-22

PRIOR APPLICATION NUMBER: 60/259,308

PRIOR FILING DATE: 2001-12-22

PRIOR APPLICATION NUMBER: 60/259,308

PRIOR FILING DATE: 2001-12-22

PRIOR APPLICATION NUMBER: 60/259,308

PRIOR FILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-12-22

PRIOR SEQ ID NOS: 14110

SOFTWARE: FASSESEQ FOR WINGONS VEFSION 4.0
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Sequence 13137, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 70, Application US/09905243 Patent No. US20020062009A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Staphylococcus aureus US-09-815-242-13137
                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.6%;
80.0%;
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                                                                           APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 80.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 13137
LENGTH: 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-905-243-70
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US-09-755-665-38

Sequence 38, Application US/0975565

Patent No. US20020107186A1

GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Taillon, Bruce E.
APPLICANT: Taillon, Bruce E.
APPLICANT: Spaderna Steven K.
APPLICANT: Spaderna NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631

CURRENT APPLICATION NUMBER: US/09/755,665

CURRENT FILING DATE: 2000-01-06

NUMBER: OF SEQ ID NOS: 118

SEQ ID NO 38

LENGTH: 228

TYPE: PRT

CRANISM: Homo sapiens

US-09-755-665-38
         Gaps
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92.6%; Score 25; DB 10; Length 228;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels
     0; Indels
 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: February 14, 2003, 11:21:29 Job time : 3.90323 secs
4; Conservative
                                                       |||:|
31 DYVLN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||::|
| 154 DYIVN 158
                                  1 DYVIN 5
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Matches
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 14, 2003, 11:12:02; Search time 5 Seconds Run on:

(without alignments) 96.134 Million cell updates/sec

US-09-701-001B-1 27 Perfect score: Title:

1 DYVIN 5 Sequence: Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues ched: 283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* Database

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		al						phycoerythrin alph	adenylate kinase (adenylate kinase (purine nucleoside	hypothetical prote	hypothetical prote	LysR family transc	leucine dehydrogen	÷	alcohol dehydrogen	alcohol dehydrogen		L-threonine 3-dehy	Glu/Leu/Phe/Val de	leucine dehydrogen	probable leucine d	leucine dehydrogen	leucine dehydrogen	spermine synthase	hypothetical prote	ical p	probable type I re
	ID	CFMWA	T06968	G45045	B35127	B47207	843779	A40007	S25318	JS0492	T44404	D69980	G81833	C90519	D86779	F83217	E84051	A44245	S51120	H71110	G75049	A87507	AI1859	B69962	E83995	S45607	S54160	10	28	E81302
	rth DB																		347 1				~	-	<+		ထ	376 2		
% Query	Match Length	0.	0.	0.	0.	100.0	100.0	0.				0.	100.0			0	0.	0.	0.		100.0	0					0	0.	0.	100.0
	Score	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27
Result	No.	Н	2	3	4	2	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

probable acyl-CoA probable fadE2 pro	gamma-glutamyl pho	leucine dehydrogen	probable PTS trans	hypothetical prote	flgK protein prote	hook associated pr	hypothetical prote	xylanase - Prevote	hypothetical prote	hypothetical prote	plasma kallikrein	hypothetical prote	hypothetical prote
D83284 E70618	A97300	A31950	T36129	H71452	A97429	AB2647	T32337	S27500	T27765	T35222	KOMSPL	AC2430	876729
2.2	(7)	7 [7	7	7	7	~	7	N	7	Н	7	7
386 403	418	429	431	488	492	492	499	584	587	610	638	703	705
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
27	27	27	27	27	27	27	27	27	27	27	27	27	27
30	12.0	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 CFWWA C-phycocyanin alpha chain - Fischerella sp. C; Species: Fischerella sp. C; Species: Fischerella sp. C; Species: Fischerella sp. C; Date: 30-Jun-1979 #sequence_revision 30-Jun-1979 #text_change 30-Apr-199 C; Jate: 30-Jun-1979 #sequence_revision 30-Jun-1979 #text_change 30-Apr-199 C; Accession: A00315 R; Frank, G.; Sidler, W.; Widmer, H.; Zuber, H. Hoppe-Seyler's Z. Physiol. Chem. 359, 1491-1507, 1978 A; Title: The complete amino acid sequence of both subunits of C-phycocyanit A; Reference number: A00315; MuID: 79087164; PMID: 103794 A; Rocession: A00315 A; Molecule type: protein A; Residues: 1-162 <fran a;="" as="" c;="" chromoprotein;="" designated="" keywords:="" laminosus="" mastigocladus="" note:="" photosynthesis;="" photosynthesis;<="" phycocyanin="" phycocyanobilin="" source="" superfamily:="" th="" the="" was=""><th>g n from the</th><th>:0</th></fran>	g n from the	:0
	RESULT 1 CFMWA C-phycocyanin alpha chain - Fischerella sp. C;Species: Fischerella sp. C;Species: Fischerella sp. C;Species: Pischerella sp. C;Species: 30-Jun-1979 #sequence_revision 30-Jun-1979 #text_change 30-Apr-1999 C;Accession: A00315 R;Frank, G.: Sidler, W.: Widmer, H.: Zuber, H. Hoppe-Seyler's Z. Physiol. Chem. 359, 1491-1507, 1978 A;Title: The complete amino acid sequence of both subunits of C-phycocyanin from the A;Reference number: A00315; MuID: 9087164; PMID:103794 A;Aocession: A00315 A;Molecule type: protein A;Residues: 1-162 <-FRRA- A;Note: the source was designated as Mastigocladus laminosus C;Superfamily: phycocyanin C;Keywords: chromoprotein; photosynthesis; phycocyanobilin F;84/Binding site: phycocyanobilin (Cys) (covalent) #status experimental	Duery Match 100.0%; Score 27; DB 1; Length 162; Sest Local Similarity 100.0%; Pred. No. 76; Aatches 5; Conservative 0; Mismatches 0; Indels 0; 1 DYVIN 5 1 DYVIN 5 155 DYVIN 159

RESULT 2

C-phycocyanin alpha chain - Cyanophora paradoxa cyanelle
C;Species: cyanelle Cyanophora paradoxa
C;Species: cyanelle Cyanophora paradoxa
C;Species: o.Apr-1999 #Sequence_revision 30-Apr-1999 #text_change 11-Jun-1999
C;Accession: T06968; A24650
R;Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A. submitted to the EMBL Data Library, July 1995
A;Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.
A;Reference number: Z15840
A;Accession: T06968

A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-162 <STI>
A;Cross-references: EMBL:U30821; NID:g1016083; PIDN:AAA81311.1; PID:g1016224
A;Experimental source: strain Pringsheim LB555
B;Lemaux, P.G.; Grossman, A.R.
EMBO J. 4, 1911-1919, 1985
A;Title: Major 1ight-harvesting polypeptides encoded in polycistronic transcripts in A;Title: Major 1ight-harvesting polypeptides encoded in polycistronic transcripts in A;Title: Major 1ight-harvesting polypeptides encoded in polycistronic transcripts in A;Titleference number: A91009; MUID:86055745; PMID:2998775
A;Accession: A24650
A;Molecule type: DNA
A;Residues: 1-15 <LEM>A;Cross-references: GB:X02790; NID:g11385; PIDN:CAA26557.1; PID:g11386
C;Genetics:

Score 27; DB 2; Length 162; Pred. No. 76;

0; Indels

Mismatches

·,

100.0%; 100.0%;

Query Match
Best Local Similarity 100.0
Matches 5; Conservative

cyanelle

A;Gene: cpcA A; Genome:

1 DYVIN 5

δ g phycoerythrin I alpha chain - Synechococcus sp. (strain WH8020)

chococcus sp. WH8020.

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phycoerythrin alpha subunit - red alga (Rhodella violacea)
C.Species: Rhodella violacea
C.Species: Rhodella violacea
C.Species: Rhodella violacea
C.Species: Barels sequence_revision 18-Nov-1994 #text_change 23-Feb-1997
C.Accession: B47207
R.Bernard, C.; Thomas, J.C.; Mazel, D.; Mousseau, A.; Castets, A.M.; Tandeau de Marsa Proc. Natl. Acad. Sci. U. S.A. 89, 9564, 9568, 1992
A.Title: Characterization of the genes encoding phycoerythrin in the red alga Rhodell A; Reference number: A47207, MuID: 93028502; PMID: 1409666
A.Accession: B47207
A.Molecule type: nucleic acid
A.Residues: 1-164 < BER>
A.Residues: 1-164 < BER>
A.Note: sequence extracted from NCBI backbone (NCBIN:115792, NCBIP:115794)
C.Superfamily: phycocyanin
C.Keywords: chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
$43779
Synyocerythrin I alpha chain - Synechococcus sp.
C; Species: Synechococcus sp.
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jun-1999
R; Newman, J; Mann, N.H.; Carr, N.G.
Plant Mol. Biol. 24, 679-683, 1994
A; Title: Organization and transcription of the class I phycoerythrin genes of the mar A; Reference number: 84377; MUID:94207193; PMID:7512390
A; Accession: 843779
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-164 < NEW>
A; Cross-references: EMBL:X72961; NID:9288983; PIDN:CAA51465.1; PID:9288986
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A;Cross-references: GB:M61118; NID:g154529; PIDN:AAA27320.1; PID:g154531; EMBL:M95288
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phycocrythrin class II alpha chain mpeA - Synechococcus sp. (strain WH8020)
c;Species: Synechococcus sp.
C;Decies: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 11-Jun-1999
C;Accession: A40007; S31048
R;Wilbanks, S.M.; de Lorimier, R.; Glazer, A.N.
J. Biol. Chem. 266, 9535-9539, 1991
A;Title: Phycocrythrins of marine unicellular cyanobacteria. Sequence of a class II p.
A;Reference number: A40007; MUID:91236722; PMID:1903390
A;Accession: A40007
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
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Pred. No. 77;
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C;Superfamily: phycocyanin
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te: 03-Aug-1990 #text_change 11-Jun-1999

R; Andersoin. B.35127 #sequence_revision 03-Aug-1990 #text_change 11-Jun-1999

R; Andersoin. L.K.; Grossman, A.R.
J. Bacteriol. 172, 1297-1305, 1990

A; Fitle: Structure and light_regulated expression of phycoerythrin genes in wild-type and A; Reference number: A35127; MUID:90170840; PMID:2106507

A; Rocession: B35127

A; Molecule type: DNA

A; Residues: 1-164 <And>
A; Residues: 1-164 <And>
A; Residues: GB:M33812; NID:g154457; PIDN:AAA27280.1; PID:g154459

C; Superfamily: phycocyanin
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                                                                              C; Superfamily: phycocyanin
C; Keywords: chromoprotein; cyanelle; heterodimer; photosynthesis; phycocyanobilin
F; 84/Binding site: phycocyanobilin (Cys) (covalent) #status predicted
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A.Accession: G45045
A.Accession: G45045
A.Accession: G45045
A.Accession: G45045
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-164 <WIL>
A.Cross-references: EMBL.M95288; NID:g154551; PIDN:AAA27340.1; PID:g154560
A.Koperimental source: WH8020
A.Note: sequence extracted from NCBI backbone (NCBIP:121981)
C.Genetics:
C.Genetics:
C.Superfamily: phycocyanin
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Query Match

100.0%; Score 27; DB 2; Length 164;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels

157 DYVIN 161

1 DYVIN 5

ò qq phycoerythrin alpha chain - Synechocystis sp. (strain PCC 6701)

Q,

100.0%; Score 27; DB 2; Length 164; 100.0%; Pred. No. 77; tive 0; Mismatches 0; Indels

5; Conservative

Best Local Similarity Matches 5; Conserv

Query Match

157 DYVIN 161

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Ŋ RESULT B47207

1 DYVIN 5

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C;Accession: T44404; C83669
C;Accession: T44404; C83669
R;Takami, H.; Takaki, Y.; Nakasone, K.; Hirama, C.; Inoue, A.; Horikoshi, K.
Biosci. Biotechnol. Biochem. 63, 452-455, 1999
A;Title: Sequence analysis of a 32-kb region including the major ribosomal protein ge
A;Reference number: 222756; MUID:99209008; PMID:10192928
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Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20512582; PMID:11058132
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A;Experimental source: strain C-125
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Frieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Saro, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Tarpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Tamakoco, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.F.; Zumatein, E.; Yoshikawa, H.; Danchin, A.
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Reference number: A69580; MUID:98044033; PMID:9384377
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A.Experimental source: strain 168
C.Genetics:
A.Genetics:
A.Generics:
A.Generics
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A;Experimental source: strain C-125
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C;Species: Bacillus halodurans
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 15-Jun-2001
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C;Superfamily: adenylate kinase
C;Keywords: AFP; P-loop; phosphotransferase
F;7-14/Region: nucleotide-binding motif A (P-loop) #status atypical
F;80-85/Region: nucleotide-binding motif B #status atypical
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A;Molecule type: DNA
A;Residues: 1-217 <TAK>
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..hos 5; Conservative
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C;Superfamily: adenylate kinase
C;Keywords: phosphotransferase
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A; Molecule type: DNA
A; Residues: 1-217 <STO>
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A; Molecule type: DNA
A; Residues: 1-99 CSUH-
A; Residues: 1-99 CSUH-
A; Residues: 1-99 CSUH-
A; Experimental source: strain Marburg; cell line PB2
A; Experimental source: strain Marburg; Caldwell, B.; Capuano, W.; Carter, N.M.; Ch
A; Experimental source: strain M.; Enjita, M.; Fujita, M.; Marburg, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
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A; Residues: 1-116 < YOS>
A; Cross-references: EMBL:M31102; NID:g1184272; PIDN:AAB59119.1; PID:g143579
A; Cross-references: strain 1A241
A; Experimental source: strain 1A241
B; Suh, J.W.; Boylan, S.A.; Thomas, S.M.; Dolan, K.M.; Oliver, D.B.; Price, C.W.
Mol. Microbiol. 4, 305-314, 1990
A; Title: Isolation of a secY homologue from Bacillus subtilis: evidence for a common pro
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N.Alternate names: ATP-AMP transphosphorylase
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: O'S-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: JS0492; S12684; S08630; E69583
R;Nakamura, R.; Nakamura, A.; Takamatsu, H.; Yoshikawa, H.; Yamane, K.
J. Blochem. 107, 603-607, 1990
A;Title: Cloning and characterization of a Bacillus subtilis gene homologous to E. coli
A;Reference number: JS0490; MuID:90292990; PMID:2113521
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Nucleic Acids Res. 18, 1647, 1990
A;Title: Sequence of the Bacillus subtilis spectinomycin resistance gene region.
A;Reference number: S12680; MUID:90221911; PMID:2139212
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C,Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 28-May-1999
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A;Residues: 1-165 <LOR>
A;Cross-references: GB:M91809; NID:g154532; PIDN:AAA27322.1; PID:g154534
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                                      Mismatches
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                                           Conservative
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| 158 DYVIN 162
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LysR family transcription regulator [imported] - Lactococcus lactis subsp. lactis (st. Cyspecies: Lactococcus lactis subsp. lactis
LysR family transcription regulator [imported] - Lactococcus lactis subsp. lactis
Cyspecies: Lactococcus lactis subsp. lactis
Cycession: D86779
RyBolotin, A:; Wnicker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A;Title: D86779
A; Reference number: A86625; MUID:21235186; PMID:11337471
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-303 <STO>
A;Cross references: GB:ABC005176; PID:912724207; PIDN:AAK05334.1; GSPDB:GN00146
A;Experimental source: strain IL1403
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C;Date: 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83217
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
R;Stover, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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A;Accession: F83217
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100.0%; Pred. No. 1.4e+02;
iive 0; Mismatches 0;
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Matches 5; Conservative
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A; Residues: 1-341 <STO>
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                                                                                                                                   purine nucleoside phosphorylase homolog yrru - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
C;Accession: D6980
C;Berder, A.; Bilbert, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Husono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Harwood, C.R.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Potteelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Desato, V.; Uchiyana, T.; Winters, P.; Winters, P.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyana, T.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyana, T.; Winters, P.; Wipat, A.; Tanamoto, H.; Yamane, K.; Yasta, K.; Yoshida, R.; Lie: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

**Minters of the Gram-positive bacterium Bacillus subtilis.**
**Minters of the Gram-positive decomes sequence of the Gr
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C; pecies: Neisseria meningitidis
C; paccession: G81833
C; Accession: G81833
C; Moule, S; Moule
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A;Residues: 1-259 <PAR>
A;Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85255.1; PID:g738066
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA2036
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-231 < KUN>
A; Residues: 1-231 < KUN>
A; Cross-references: GB: 299117; GB: AL009126; NID: 92634966; PIDN: CAB14669.1; PID: 92635173
A; Experimental source: strain 168
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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C;Superfamily: Escherichia coli pfs protein
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Best Local Similarity
Matches 5; Conserv
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69 DYVIN 73
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A; Experimental source: strain PAO1
C; Genetics:
A; Gene: ldh; PA3418
C; Genetics:
C; Genetics:
A; Gene: ldh; PA3418
C; Superfamily: leucine dehydrogenase
C; Superfamily: leucine dehydrogenase
Query Matches
C; Conservative
C; Mismatches
C; Conservative
C; Mismatches
C; Conservative
C; Mismatches
C; Local Similarity
C; Mismatches
C; Conservative
C; Mismatches
C; Conservative
C; DYVIN 5
C; Conservative
C; Mismatches
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C; Conservat
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Search completed: February 14, 2003, 11:19:44 Job time : 6 secs

; 0

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 14, 2003, 11:05:27; Search time 2.58065 Seconds (without alignments) 80.360 Million cell updates/sec Run on:

US-09-701-001B-1 1 DYVIN 5 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues ched: 112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	DOS730 cvanonhora	D00303	MASON AND MANAGEMENT OF THE PROPERTY OF THE PR	002179	036005	RHOVL Q02036	P20778	P27646	P37720	P38372	P16304	032028	E 068955	P39462	P50381	I Q53560	J P54531	059194	060030	P52788	P97355	P13154	097e62	011076	009374	P26262	086Z6Ö	I P13466	. p26190	FREDI P1487	PORDH PS1368 porphyra	00101
5	ΩI	4000	4000	ח לאום	PHAI	PHEA	PHEA	PHEA	PHA2	PHA2_	KAD BACHD	KAD_BACSU	MTN BACSU	ANFD	ADH SULSO	ADH_SULSR	DHLE	DHLE	DHLE	DHLE	SPSY	SPSY	DHLE	PROA	YWV2	YS48	KAL	SYL	GELA	RRPO	PHA3_1	PHEA	
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CARP_POLTU	VDH_STRCM OMPF ECOLI	VDH_STRAL	VDH_STRCO	VDH_STRFR	PGK_PYRAB	PGK_PYRHO	EXUT_ECOL!	AMY2_DICTH	ILVB_LACLA	YHZ6_YEAST
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96.3	96.3	96.3	96.3	96.3	96.3	96.3	96.3	96.3	96.3	8.96
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34	35	37	38	39	40	41	42	43	44	45

ALIGNMENTS	RESULT. PROF. CYARA DIA PREC. CYARA DEC. CYARA DE
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                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-79087164; PubMed-103794;
Frank G., Sidler W., Widmer H., Zuber H.;
The complete amino acid sequence of both subunits of C-phycocyanin from the cyanobacterium Mastigocladus laminosus.";
If the cyanoterium Mastigocladus laminosus.";
I- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN FROM THE PHYCOBLILPROTEIN COMPLEX.
InterPro; IPR001659; Phycobilisome.
Pfam; PF00502; Phycobilisome; 1.
ProDom; PD000340; Phycobilisome; 1.
Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P00306; 1PHN. InterPro. PROD1599. Phycobilisome. Pf0502: Phycobilisome. ProD0m; PF00502: Phycobilisome; ProD0m; PD000340; Phycobilisome; 1. Phycobilisome; Electron transport; Photosynthesis; Bile pigment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structure and molecular evolution of the gene cluster encoding proteins of the rod substructure of the phycobilisome from the cyanobacterium Mastigocadus laminosus."; Submitted (JAN-1992) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                 100.0%; Score 27; DB 1; Length 162; 100.0%; Pred. No. 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-!- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
                                                                                              PHYCOCYANOBILIN CHROMOPHORE
                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Kufer W., Hoegner A., Eberlein M., Mayer K., Buchner A.,
Gottschalk L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHYCOCYANOBILIN CHROMOPHORE.
                                                                                                             (BY SIMILARITY).
30BA91A389036AF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 67 TT -> LI (IN REF. 2).
162 AA; 17392 MW; B19F9856EA51E4AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mastigocladus laminosus (Fischerella sp.).
Bacteria; Cyanobacteria; Stigonematales; Fischerella.
NCBI_TaxID=1191;
                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                        100.0%; Pred. nc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                            162 AA; 17512 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   C-phycocyanin alpha chain.
                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                            84
                                                                                                                                                                                   Sest Local Similarity
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Best Local Similarity
Matches 5; Conserv
                                                                                            84
                                                                                                                                                                                                                                                                       155 DYVIN 159
                                                                                                                                                                                                                                  1 DYVIN 5
                                                                                                                                                                                                                                                                                                                                                            PHCA_MASLA
P00307;
                                                                        Cyanelle.
                                                                                                                            SEQUENCE
                                                                                                                                                                 Query Match
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SEQUENCE
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Pfam; PF00502; Phycobilisome; 1.
ProDom; PD000340; Phycobilisome; 1.
Phycobilisome; 1.
Phycobilisome; Electron transport; Photosynthesis; Bile pigment.
BINDING 82 PHYCORYTHROBILIN CHROMOPHORE.
BINDING 139 139 PHYCORYTHROBILIN CHROMOPHORE.
SEQUENCE 164 AA; 17853 MW; B443CFD08C859D6A CRC64;
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                                                                                                                                                                                                                                                                         Synechococcus sp. (strain WH7803).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synechococcus sp. (strain WH8020).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBL_TaxID=32052;
                                                                                                               01-007-1994 (Rel. 30, Created)
01-00T-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-phycoerythrin class I alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUN-2002 (Rel. 41, Last annotation update)
C-phycoerythrin class I alpha chain.
                                                                   164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=94207193; Pubmed=7512390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X72961; CAA51465.1; -.
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Best Local Similarity 100.v
                                                               STANDARD;
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PIR; S43779; S43779.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 DYVIN 161
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                                                      PHA1_SYNPW
Q08086;
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Q02179;
                               PHA1_SYNPW
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RESULT 3
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Gaps

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SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
SUBCELLULAR LOCATION: WITHIN THE THYLAKOID LUMEN. PERIPHERY OF THE RODS OF THE PHYCOBILISOME.
                                                        -!- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
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BINDING 82 82
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HSSP; 036005; 1B8D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhodella violacea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 DYVIN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DYVIN 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CPEA OR RPEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHEA_RHOVL
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              002036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHEA_RHOVL
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  Db
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                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                      MEDLINE-93123238; PubMed-8419325; Wilbanks S.M., Glazer A.N.; Wilbanks S.M., Glazer A.N.; Rod structure of a phycocrythrin II-containing phycobilisome. I. Organization and sequence of the gene cluster encoding the major phycobiliprotein rod components in the genome of marine Synechococcus
                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. SUBCELLULAR LOCATION: Periphery of the rods of the phycobilisome. PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN FROM THE PHYCOBILIPROTEIN COMPLEX.
                                    de Lorimier R., Wilbanks S.M., Glazer A.N.; "Genes of the R-phycocyanin II locus of marine Synechococcus spp., and comparison of protein-chromophore interactions in phycocyanins
                                                                                                                                                                                                                                                                                J. Biol. Chem. 268:1226-1235(1993).
-!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN FROM THE PHYCOBILIPROTEIN COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Crystal structure of a phycourobilin-containing phycoerythrin at 1.90-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR001659; Phycobilisome.
Pfam; PF00502; Phycobilisome; 1.
ProDom; PD000340; Phycobilisome; 1.
Phycobilisome; Electron transport; Photosynthesis; Bile pigment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Ceramiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ritter S., Hiller R.G., Sharples F.P., Wrench P.M., Welte W Diederichs K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 27; DB 1; Length 164; 100.0%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHYCOERYTHROBILIN CHROMOPHORE.
PHYCOERYTHROBILIN CHROMOPHORE.
7AED0B19EDF5D2C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-phycocrythrin alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                differing in bilin composition."; Plant Mol. Biol. 21:225-237(1993).
                      MEDLINE=93144698; PubMed=8425055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 AA; 17860 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M95288; AAA27340.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; G45045; G45045.
PIR; S31055; S31055.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; 036005; 1B8D.
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=42003;
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139
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| 157 DYVIN 161
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BINDING BINDING

PHEA_GRIMO RESULT 5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bernard C., Thomas J.C., Mazel D., Mousseau A., Castets A.M.,
Tandeau de Marsac N., Dubacq J.P.;
"Characterization of the genes encoding phycoerythrin in the red alga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- FUNCTION: LIGHT-HARVESTING PHOTOSYNHETIC BILE PIGMENT-PROTEIN
FROM THE PHYCOBILIPROTEIN COMPLEX.
-1- SUBUNIT: HETEROPOLYMER OF 6 ALPHA, 6 BETA AND ONE GAMMA CHAINS.
-1- SUBCELLULAR LOCATION: Periphery of the rods of the phycobilisome.
-1- STREELLULAR LOCATION: Periphery of the rods of the phycobilisome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhodella violacea: evidence for a splitting of the rpeB gene by an
                                                                                                                                                                                                                                                                                                                                                                                                               PDB; 188D; 18-FEB-99.
InterPro; IPR001659; Phycobilisome.
Pfam; PF00502; Phycobilisome; 1.
Probom; PD00340; Phycobilisome; 1.
Probom; Electron transport; Photosynthesis; Bile pigment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 27; DB 1; Length 164;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHYCOERYTHROBILIN CHROMOPHORE. 139 139 PHYCOERYTHROBILIN CHROMOPHORE. 164 AA; 17669 MW; EFCF110AF760201A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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Matches
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0
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-1- SUBCELLULAR LOCATION: Periphery of the rods of the phycobilisome.
-1- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90170840; PubMed=2106507; Anderson L.K., Grossman A.R.; "Structure and light-regulated expression of phycoerythrin genes in wild-type and phycobilisome assembly mutants of Synechocystis sp. strain PCC 6701.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 172:1297-1305(1990).
-!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN FROM THE PHYCOBILIPROTEIN COMPLEX.
           Pfam; PF00502; Phycobilisome; 1.
ProDom; PD000340; Phycobilisome; 1.
Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSF; .....
InterPro; IPR001659; Fulycocc.
Pfan: PF00502; Phycobilisome; 1.
ProDom: PD000340; Phycobilisome; 1.
Phycobilisome; Electron transport; Photosynthesis; Bile pigment.
Phycobilisome; Ilaq PHYCOENTHROBILIN CHROMOPHORE.
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0
                                                                                                                   100.0%; Score 27; DB 1; Length 164; 100.0%; Pred. No. 25; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 27; DB 1; Length 164; 100.0%; Pred. No. 25; tive 0; Mismatches 0; Indels
                                                                             139 139 PHYCOERYTHROBILIN CHROMOPHORE. 164 AA; 17696 MW; 6E8494D18B8204FC CRC64;
                                                                  PHYCOERYTHROBILIN CHROMOPHORE.
                                                                                                                                                                                                                                                                                                                                               CPEA OR CPAA.
Synechocystis sp. (strain PCC 6701).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                        01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-phycoerythrin alpha chain.
                                                                                                                                                                                                                                                                     164 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; 036005; 1B8D.
InterPro; IPR001659; Phycobilisome.
InterPro; IPR001659; Phycobilisome
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                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1144;
                                                                                                                                                                                       157 DYVIN 161
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                                                                                                                                                                        1 DYVIN 5
                                                    Chloroplast.
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                                                                                                                                                                                                                                                                  PHEA_SYNY1
P20778;
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                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=91236722; PubMed=1903390; Wilbanks S.M., de Lorimier R., Glazer A.N.; "Phycoerythrins of marine unicellular cyanobacteria. III. Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phycoerythrins.";

J. BAOL. Chem. 266:9215-9527(1991).

-!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN FROM THE PHYCOBILIPROTEIN COMPLEX.

-!- SUBGUILT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

-!- SUBCELLULAR LOCATION: Periphery of the rods of the phycobilisome.

-!- PTM: CONTAINS THREE COVALENTLY LINKED BILIN CHROMOPHORES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ong L.J., Glazer A.N.; "Phycoerythrins of marine unicellular cyanobacteria. I. Bilin types
                                                                                                                                                                                                                                                                                                                                                                                                                          de Lorimier R., Wilbanks S.M., Glazer A.N.;
"Genes of the R-phycocyanin II locus of marine Synechococcus spp.,
and comparison of protein-chromophore interactions in phycocyanins
differing in bilin composition.",
Plant Mol. Biol. 21:225-237(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Electron transport; Photosynthesis; Bile pigment.

7 PHYCOUROBILIN CHROMOPHORE.

7 PHYCOERVTHROBILIN CHROMOPHORE 1.

9 140 PHYCOERVTHROBILIN CHROMOPHORE 2.

AA; 17670 MW; B17A9C0BA5D24602 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and locations and energy transfer pathways in Synechococcus spp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                   Synechococcus sp. (strain WH8020).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-phycoerythrin class II alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a class II phycoerythrin.";
J. Biol. Chem. 266:9535-9539(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHROMOPHORES, AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=93144698; PubMed=8425055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91236720; PubMed=1903388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M95288; AAA27333.1; -. EMBL; M61118; AAA27320.1; -.
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      STANDARD:
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PIR, S31048, S31048.
HSSP, O36005, 1BBD.
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165 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=32052;
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Phycobilisome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DYVIN 5
PHA2_SYNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a class II
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SEQUENCE
                                 P27646;
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NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DYVIN 5
                                                                                    Fuji F., Hira
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAD_BACSU
P16304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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STRAIN-C-125 / JCM 9153;

MEDLINE=99209008; PubMed=10192928;

Takami H., Takaki Y., Nakasone K., Hirama C., Inoue A., Horikoshi K.;

Takami H., Takaki Y., Nakasone K., Hirama C., Inoue A., Horikoshi K.;

Takami H., Takaki Y., Nakasone T., Inoue A., Horikoshi K.;

Takami H., Takaki Y., Nakasone A., Horikoshi K.;

Takami H., Takaki J., Hirami L., Horikoshi K.;

Protein gene clusters from alkaliphilic Bacillus sp. strain C-125.";

Biosci. Biotechnol. Biochem. 63:452-455(1999).
                                                                                                                                                                                                                                                                                                                                                                                                FROM THE PHYCOBILLIPROTEIN COMPLEX.
-!- SUBBURIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-!- SUBCELLULAR LOCATION: Periphery of the rods of the phycobilisome.
-!- PTM: CONTAINS THREE COVALENTLY LINKED BILLIN CHROMOPHORES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE-30004402.; PubMed-1391782;

MEDLINE-30004402.; Chen C.-C.J., Glazer A.N.;

Gequence comparison of two highly homologous phycoerythrins

"Sequence comparison of two highly homologous phycoerythrins

"Sequence comparison of two highly homologous phycoerythrins

"Sequence comparison of two highly homologous

"Influence of two highly homologous phycoerythrins

"Influence of two highly highly homologous phycoerythrins

"Influence of two highly homologous phyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPRO1659; Phycobilisome.

Fran, PF00502; Phycobilisome; 1.

Probom; PD000340; Phycobilisome; 1.

Phycobilisome; Electron transport; Photosynthesis; Bile pigment.

Phycobilisome; Bietron transport; PhycouroBILIN CHROMOPHORE 1.

BINDING 83 PHYCOUROBILIN CHROMOPHORE 2.

BINDING 140 140 PHYCOUROBILIN CHROMOPHORE 3.

SEQUENCE 165 AA; 17729 MW; DBD252CC5DD39B2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAD_BACHD STANDARD; PRT; 217 AA.
P38372; Q9WWJ3; Q9JPW7;
01-0cT-1994 (Rel. 30, Created)
6-0cT-2001 (Rel. 40, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphorylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 27; DB 1; Length 165; 100.0%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                              Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=29410;
                                                   01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-phycoerythrin class II alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
              PRT; 165 AA.
                                                                                                                                                                  Synechococcus sp. (strain WH8103).
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165 AA; 17729 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M91809; AAA27322.1; -.
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              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S25318.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; 036005; 1B8D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 DYVIN 162
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                  PHA2_SYNPZ
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                                                                                                                                      "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                         STRAIN-C-125 / JCM 9153;

MEDLINE-92881482; PubMed-1512566;

Kang S.K., Kudo T., Horikoshi K.;

Molecular cloning and characterization of an alkalophilic Bacillus
"Molecular cloning and characterization of an alkalophilic Bacillus
"Molecular cloning and characterization of an alkalophilic Bacillus
sp. 0125 gene homologous to Bacillus subtilis secY.";
J. Gen. Microbiol. 138:1365-1370(1992).

-!- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
MAINTENNACE AND CELL GROWTH.

-!- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakamura K., Nakamura A., Takamatsu H., Yoshikawa H., Yamane K.;
                                          Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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01-FBE-1991 (Rel. 17, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase)
(Superoxide-inducible protein 16) (SOI16).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBUNIT: MONOMER.
-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- SUBCELLULARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I -> N (IN REF. 3).
FD5DF854B3BA3592 CRC64;
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PROSITE; PSO0113; ADENYLATE, TRIASE; 1.
TYANGSFARSE; Kinase; ATP-binding; Complete proteome.
NP BIND 7 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P27142; 1ZIN.
InterPro; IPRO00850; Adenylate_kin.
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MEDLINE=90292990; Pubmed=2113521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00406; adenylatekinase; 1.
STEAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed=11058132;
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EMBL; AP001507; BAB03874.1; --
EMBL; D10360; BAA01192.1; --
PIR; C44859; C44859.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PR00094; ADENYLTKNASE
                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-107 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
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Matches

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                                                                                                                                                                                                                                                                                                                                               Price C.W.; "Isolation of a secY homologue from Bacillus subtilis: evidence for a common protein export pathway in eubacteria."; Mol. Microbiol. 4:305-314(1990).
 "Cloning and characterization of a Bacillus subtilis gene homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              First steps from a two-dimensional protein index towards a response-
                                                                       STRAIN-168 / Marburg;
MEDLINE-96186897; PubMed-8635744;
Suh J.W., Boylan S.A., Oh S.H., Price C.W.;
"Genetic and transcriptional organization of the Bacillus subtilis
                                                                                                                                                                               SEQUENCE OF 1-116 FROM N.A.
MEDLINE-90221911; PubMed-2139212;
Yoshikawa H., Doi R.H.;
"Sequence of the Bacillus subtilis spectinomycin resistance gene
                                                                                                                                                                                                                                                                                                                                  Suh J.W., Boylan S.A., Thomas S.M., Dolan K.M., Oliver D.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=168 / IS58;
MEDIINE-97443988; PubMed=9298659;
Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- INDUCTION: BY SUPEROXIDE.
-!- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probom; PD000657; Adenylate_Kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE; 1.
Transferase; Kinase; ATP-binding; Complete proteome.
NP_BIND 7 15 ATP (BY SIMILARITY).
SEQUENCE 217 AA; 24119 MW; ECB9ECF4F26A1E90 CRC64;
                                                                                                                                                                                                                                                        Nucleic Acids Res. 18:1647-1647(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P27142; IZIN.
SubtiList; BG10446; adk,
InterPro; IPR000850; Adenylate_kin.
Pfam; PF00406; adenylatekinase; 1.
                                                                                                                                                                                                                                                                                                                MEDLINE=90251170; PubMed=2110998;
                            Biochem. 107:603-607(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR00094; ADENYLTKNASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D00619; BAA00496.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L47971; AAB06820.1;
EMBL; M31102; AAB59119.1;
EMBL; X51329; CAA35713.1;
EMBL; Z99104; CAB11913.1;
                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-99 FROM N.A.
                                                                                                                                      spc-alpha region.";
Gene 169:17-23(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; JS0492; JS0492.
PIR; S08630; S08630.
PIR; S12684; S12684.
                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-20.
                    coli secY
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RA Azevedo V., Bertero M.G., Beseieres P., Bolotin A., Brochert S.,
RA Deuriss R., Deursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Borniss R., Deursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Burschi C.V., Caldwell B., Capunno V., Carter N.M.,
RA Denizot F., Devine K.M., Dusterhoft A., Fahrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Glims S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Gliseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kobayashi Y., Koetter P., Koningstein G., Kroph S., Kumano M.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Kumano M.,
RA Parro V., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Raccan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Schloich S., Schroeter R., Scoffone F.,
RA Scookin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Yananoto K., Yata K.,
Nuhrers P., Wibat A., Yamanoto M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Weller E., Wedler E., Wedler E., Weller E., Wedler E., Weller E., Weller E., Wedler E., Weller E., We
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997).
-!- FUNCTION: RESPONSIBLE FOR CLEAVAGE OF THE GLYCOSIDIC BOND IN BOTH 5'-METHYLTHIOADENOSINE (MTA) AND S-ADENOSYLHOMOCYSTEINE (SAH) (BY
                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
MTA/SAH nucleosidase [Includes: 5'-methylthioadenosine nucleosidase (EC 3.2.2.16); S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)0 = adenine +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: Methylthioadenosine + H(2)0 = adenine + 5-
                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
               0;
       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE MIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S-D-ribosyl-L-homocysteine.
5; Conservative
                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methylthio-D-ribose.
                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                             108 DYVIN 112
                                                 1 DYVIN 5
                                                                                                                                                                                                                           MTN_BACSU
                                                                                                                                                                      RESULT 12
MTN_BACSU
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EMBL; 299117; CAB14669.1; -.

Length 217;

DB 1;

100.0%; Score 27; DB 100.0%; Pred. No. 33;

Ouery Match
Best Local Similarity

DR DR DR KW SQ

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158 DYVIN 162
                                                      RESULT 14
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                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Nitrogenase iron-iron protein alpha chain (EC 1.18.6.1) (Nitrogenase component I) (Dinitrogenase 3 alpha subunit) (Fragment).
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Clostridia; Clostridiales; Heliobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                              Score 27; DB 1; Length 231; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31772 MW; CDF25376AF1056A1 CRC64;
Subtilist; BG13800; mtn.
InterPro; IPR000845; PNP_UDP.
Pfam; PF01048; PNP_UDP-1; 1.
ProDom; PD003928; PNP_UDP: 1.
Hydrolase; Wullifunctional enzyme; Complete proteome.
SEQUENCE 231 AA; 25264 MW; 7F6B8BC8EDA1E728 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; Nitrogen fixation; Iron-sulfur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF058785; AAC14342.1; -.
HSSP; P00467; IMIO.
InterPro: IPR0001318; Nitrognse_compl.
InterPro; IPR000510; Oxred_nitrognse1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00148; oxidored_nitro; 1
                                                                                                 100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 Heliobacterium gestii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 AA;
                                                                                                             Best_Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2699;
                                                                                                                                                                                                                                                                                                                                                                                                            Heliobacterium.
                                                                                                                                                                                     69 DYVIN 73
                                                                                                                                                           1 DYVIN 5
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068955;
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SEQUENCE
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                                                                                                                                                                                                                                   RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: HOMODIMER AND HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Thermostable NAD(+)-dependent alcohol dehydrogenase from Sulfolobus solfataricus: gene and protein sequence determination and relationship to other alcohol dehydrogenases."; Biochemistry 31:12514-12523(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone
ADH_SULSO STANDARD; PRT; 347 AA.
P39462; 074076;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
NAD-dependent alcohol dehydrogenase (BC 1.1.1.1).
ADH OR $S02536.
Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ammendola S., Raia C.A., Caruso C., Camardella L., D'Auria S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; Zinc; NAD; Methylation; Complete proteome. MOD_RES 11 11 METHYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- COFACTOR: ZINC; BINDS 4 ZINC IONS PER DIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METHYLATION
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-ATCC 35092 / DSM 1617 / P2;
MEDLINE-93099126; PubMed=1463738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002085; Adh_zn_family.
InterPro; IPR000051; SAM_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC 35092 / DSM 1617 / P2;
Aravalli R.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATCC 35092 / DSM 1617 / P2;
MEDLINE-21332296; Pubmed-11427726;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00107; adh_zinc; 1.
PROSITE; PS00059; ADH_ZINC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002328; ADH_zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S51211; AAB24546.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   de Rosa M., Rossi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A44245; A44245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2287;
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                                                                                                                                                                                                                                                                                                                     Sulfolobus
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96122563; PubMed=8550434; Canding R., Bartolucci S.; Cannio R., Fiorentino G., Carpinelli P., Rossi M., Bartolucci S.; Clanio R., Poverexpression in Escherichia coli of the genes encoding NAD-dependent alcohol dehydrogenase from two Sulfolobus species."; J. Bacteriol. 178:301-305(1996).
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: 2INC; BINDS 4 ZINC IONS PER DIMER.
-!- SUBUNIT: HOMODIMER AND HOMOTETRAMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (SECOND ATOM) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
MY; 755848A249D4F4A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METHYLATION (BY SIMILARITY).
METHYLATION (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (SECOND ATOM) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
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0
                                                                                                                                  100.0%; Score 27; DB 1; Length 347; 100.0%; Pred. No. 54; tive 0; Mismatches 0; Indels
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01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
NAD-dependent alcohol dehydrogenase (EC 1.1.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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MOD_RES 213 213 METHYLATIO
MOD_RES 213 213 ZINC (CAPA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002338; ADB_zinc.
InterPro; IPR002085; Adb_za_family.
InterPro; IPR000051; SAM_bind.
Pfam; PF00107; adb_zinc; 1.
PROSITE; PS000059; ADH_ZINC; 1.
                                                                                                    37568 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (strain RC3)
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                    STANDARD;
 68
98
101
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Best Local Similarity
5; Conserve
68
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347 AA;
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347 AA;
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Best Local Similarity
Matches 5; Conserv
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218 DYVIN 222
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ADH_SULSR
ID ADH_SULSR
                                                                                                  SEQUENCE
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Gaps

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0; Indels

Conservative

Score 27; DB 1; Length 347; Pred. No. 54;

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218 DYVIN 222
1 DYVIN 5
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GenCore version 5.1.3
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                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                             671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                     Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
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1: sp_archea:*
2: sp_bacteria:*
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Maximum DB seq length: 2000000000
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sp_rodent:*
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sp_mhc:*
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                                                                                                                                                                                                                                                Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	0914g6 streptococc	Q9vev5 drosophila	Q9v965 drosophila	Q9emy1 amsacta moo	Q8u241 pyrococcus	Q9mj64 physarum po	Q9r282 mus musculu	Q9rqw0 neisseria m	Q98i60 rhizobium l	Q98rf0 mycoplasma	Q9cg74 lactococcus	Q9hyi7 pseudomonas	Q9k7z4 bacillus ha	Q96xe0 sulfolobus		Q9uyx0 pyrococcus
	QI	Q9L4G6	Q9VEV5	09V965	Q9EMY1	Q8U241	Q9MJ64	Q9R282	Q9RQW0	098160	Q98RF0	Q9CG74	Q9HY17	Q9K7Z4	Q96XE0	058389	08uxx0
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	Query Match Length DB	82	113	149	185	197	231	258	259	298	299	303	341	345	347	348	348
ф	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27
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OBUZ59 pyrococcus Q9uqs1 homo sapien Q9d51 caulobacter Q8xzn1 anabaena sp O85768 legionella Q9yh95 tetraodon f Q9yh96 tetraodon f Q9yh96 brachydanio Q9y85 bachylusco Q8rn27 campylobact Q8rn27 campylobact Q9prb8 campylobact Q9prb8 campylobact Q9prb8 campylobact Q9prb8 campylobact Q9prc9 trypanosoma P96831 mycobacteri Q8xxu3 ralstonia s Q9cxx7 pasteurella Q9cxx9 pasteucella Q9cxx9 satreptooncc Q01607 caenorhabdi O58017 pyrococcus Q8uhv4 agrobacteri Q8uhv4 agrobacteri	Q9v7r9 drosophila Q45397 prevotella Q97b15 thermoplasm Q86712 streptomyce Q9v7p8 drosophila
7 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	5 17 16 5
27 100.0 27 100.0	
11110000000000000000000000000000000000	44 44 44 5

ALIGNMENTS

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Guedon G., Bourgoin F., Pebay M., Roussel Y., Colmin C., Simonet J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization and distribution of two insertion sequences, IS1191 and iso-IS981, in Streptococcus thermophilus: does intergeneric transfer of insertion sequences occur in lactic acid bacteria co-
                                                                                                                                                                                                                                      Streptococcus thermophilus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococcaceae; Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roussel Y., Bourgoin F., Guedon G., Pebay M., becaris B.; "Analysis of the genetic polymorphism between three Streptococcus thermophilus strains by comparing their physical and genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20208895; PubMed=10742276;
Burrus V., Roussel Y., Decaris B., Guedon G.;
"Characterization of a novel integrative element, ICEStl, in the lactic acid bacterium streptococcusthermophilus.";
Appl. Environ. Microbiol. 66:1749-1753(2000).
                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                82 AA.
                                                   PRT;
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MEDLINE-95379495; PubMed-7651138;
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                                                   PRELIMINARY;
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SEQUENCE FROM N.A.
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RESULT 1
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Gaps

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0; Indels

Mismatches

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Conservative

1 DYVIN 5 5;

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Local Similarity

Matches

100.0%; Score 27; DB 5; Length 113; 100.0%; Pred. No. 1.2e+02;

113 AA; 13685 MW; 1943154ABADB2926 CRC64;

SEQUENCE Query Match

SO

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon C.C., Rogers Y.H.C., Blazej R.G., Change M., Pefeiffer B.D.,
RA Brail J.F., Agbayani A. An H.J., Andrews-Pennkoch C. Baldwin D.
RA Ballew R.M., Basu A., Baxendale J., Bayrakarzoglu L., Beasley E.M.,
RA Beason K.W., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchen M.R., Bouck J., Brotstein P., Bottier P.,
RA Borkova D., Botchen M.R., Bouck J., Brotstein P., Bottier P.,
RA Borkova D., Botchen M.R., Baun A., Battler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawlesy S., Dahlke C., Davanport L.B., Davies P.,
RA Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferricra S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferricra S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferricra S., Fleischmann W.,
RA Durbin K.J., Wong F. Gorrell I.M., Glasser K.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Mount S.M., Moy M., Wurphy B., Murphy L., Muzny D.M., Nelson D.L.
RA Bazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Nese M.
Shier E., Spradling A.C., Stapleton M., Stupski M.P., San H.,
RA Shue B.C., Siden-Klamos I. Stapleton M., Stupski M.P., San K.
RA Shier E., Spradling A.C., Stapleton M., Stupski M.P., San K.
RA Shier E., Spradling A.C., Stapleton M., Stupski M.P., San K.
RA Shier E., Spradling A.C., Stapleton M., Stupski M.P., Wassenbach J.,
RA Shier E., Spradling A.C., Stapleton M., Stupski M. Wassenbach J.,
RA Shier E., Spradling A.C., Stapleton M., Stupski M., Wassenbach J.,
RA Shier E., Spradli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                           Gaps
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0
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                                                                                                                                                                                     0; Indels
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                          113 AA.
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                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Best Local Similarity
Matches 5; Conserv
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NCBI_TaxID=7227;
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Respublication of the control of the
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila,
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                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CG13437 protein.
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Pred. No. 1.6e+02;
                                                                                                                         149 AA.
                                                                                                                         PRT;
                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
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Best Local Similarity
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54 DYVIN 58
                                                                                                                                           Q9V965;
                                                                                                                                                                                                                                               CG13437
                                                                                                                   09V965
                                                                              RESULT 3
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PRELIMINARY;
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| 154 DYVIN 158
                                                                                                                                                Mitochondrion.
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18 DYVIN 22
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Q9R282
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   Gaps
                                                                                                                                                                              Amsacta moorei entomopoxvirus (AmEPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
                                                                                                                                                                                                                                                                                   "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus: Analysis and Comparison with Other Poxviruses."; Virology 274:120-139(2000).
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Moyer R.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 27; DB 17; Length 197; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 27; DB 12; Length 185; 100.0%; Pred. No. 2e+02; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=VOI. DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
Wheiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AE010212; AAL81133.1;
Hypothetical protein; Complete protecome.
SEQUENCE 197 AA; 23432 MW; 516CB4985B1E083B CRC64;
   Indels
                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                         EMBL, APS 0284; AAG 02774 1; -
SEQUENCE 185 AA; 21994 MW; FD9F960A83DFF033 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein PF1009.
                                                                                                                Q9EMY1;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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    0; Mismatches
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Best Local Similarity luv..
'..c 5; Conservative
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     Conservative
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                                                                                                                                                                                                                    NCBI_TaxID=28321;
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                                      114 DYVIN 118
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                         1 DYVIN 5
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     Matches
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Q9EMY1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takano H., Abe T., Sakurai R., Moriyama Y., Miyazawa Y., Nozaki H., Kawano S., Sasaki N., Kuroiwa T.; mitochondrial genome of Physarum polycephalum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                       Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
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258 AA; 29165 MW; 742A778011ACC8D2 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
Spermine synthase (Fragment).
                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 AA.
231 AA
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Pfam; PF01564; Spermine_synth; 1.
PROSITE; PS01330; SPERMIDINE_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Gen. Genet. 264:539-545(2001).
EMBL; AB027295; BAB08098.1; -.
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                          Physarum polycephalum (Slime mold).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=129/SVJ;
MEDLINE=21106296; PubMed=11160858;
PRT;
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                    Gaps
                                                                                                                                                                                                                 Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaneko T., Nakamura 2010, 7012.1900, Watanabe A., Nakamura E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mosorhizobium loti.";

Mesorhizobium loti.";

EMBL; AP003000; BAB49656.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 27; DB 16; Length 259; 100.0%; Pred. No. 2.8e+02; Live 0; Mismatches 0; Indels (
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FC2AD5234C6E4CBE CRC64;
                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2001 (TTEMBLrel. 18, Created)
01-0CT-2001 (TTEMBLrel. 18, Last sequence update)
01-JUN-2002 (TTEMBLrel. 21, Last annotation update)
Probable transcriptional regulator.
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0
      Pred. No. 2.8e+02;
                                                                                                                                259 AA.
100.0%; Pred. ...
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                                                                                                                                                                                                                                                                             STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE-20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                       meningitidis 22491...
Nature 404:502-506(2000).
EMBL; AF058689; AAF06687.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 259 AA; 29564 MW; FC2AD5234
                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                PRELIMINARY;
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  Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          NCBI_TaxID=65699;
                                                                                                                                                                                                       FOUS OR NMA2036.
                                                        214 DYVIN 218
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78 DYVIN 82
                                        1 DYVIN 5
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                                                                                                                                            Q9RQW0;
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Q98160
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Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of the murine respiratory pathogen
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                                                                                                                                                                                                                Length 298;
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MEDLINE=21235186; PubMed=11337471;
Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                               298 AA; 33459 MW; 2D9176927BEB7DE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Complete proteome.
SEQUENCE 299 AA: 35162 MW; F932B224FC7CC801 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical protein MYPU_0590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
LySR family transcriptional regulator.
RLRA OR LL1236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 27; DB 16; 100.0%; Pred. No. 3.3e+02;
                                              Pfam; PF00126; HTH 1: 1.
Pfam; PF03466; LysR_substrate; 1.
PRINTS; PR00039; HTHLYSR.
PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 AA.
                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 29:2145-2153(2001).
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InterPro; IPR000847; HTH_LysR.
InterPro; IPR005119; LysR_subst.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL445563; CAC13232.1; -. MypuList; MYPU_0590; -.
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                                                                                                                                                                                                                                                     5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma pulmonis.
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                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                        Complete proteome. SEQUENCE 298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                           11111
245 DYVIN 249
                                                                                                                                                                                                                                                                                               1 DYVIN 5
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                                                                                                                                                                                                           Query Match
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NCBI_TaxID=86665;
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                                                                                                                                                                                                                                                                                                                                                                                         Horikoshi K.;
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SEQUENCE FROM N.A.

SEQUENCE 5592 / PAOL;

MEDINB=2043337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

A stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

A darber R.L., Golltry L., Tolentino E., Westbrock andama S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

Ropportunistic pathogen."

In Paper Sequence of Pseudomonas aeruginosa PAOL, an

Opportunistic pathogen."

In Rature 406:959-94(2000).

Rembl. ARGO6806.1;

Rembl. ARGO6806.1;
                       "The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis 11.731-753(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                      -i. SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
BMBL; ABC06355, ARK05334.1; -
InterPro; IPR00847; FFLLysR.
InterPro; IPR005119; LysR_subst.
InterPro; IPR002109; LysR_subst.
Pfam; PF00426; FFTL1; 1.
Pfam; PF00466; LysR_substrate; 1.
Print: PF03466; LysR_substrate; 1.
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 303;
                                                                                                                                                                                                                                                                                                       PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
DNA-binding; Transcription regulation; Complete proteome.
SEQUENCE 303 AA; 34906 MW; 79FF10A56F6C8983 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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SEOUENCE 341 AA; 35633 MW; ECCB810C13BF0B40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OJARA-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2007 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·;
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 27; DB 16;
100.0%; Pred. No. 3.3e+02;
iive 0; Mismatches 0;
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Weissenbach J., Ehrlich S.D., Sorokin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
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Pfam; PF02812; GLFV_dehydrog_N; 1.
PRINTS; PR00082; GLFDHDRGNASE.
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Matches 5; Conservative
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atches 5; Conservative
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LDH OR PA3418.
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277 DYVIN 281
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Q9K7Z4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

EMBL; AP001518; BAB06932.1; -
Hypothetical protein; Complete protecome.

SEQUENCE 345 AA; 38740 MW; 938F7707056F598E CRC64;
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                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
STRAIN=C-125 / JCM 9153;
STRAIN=C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                     Bacillus halodurans.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Bacillaceae; Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 27; DB 16; Length 345; 100.0%; Pred. No. 3.8e+02;
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PROSTIE; PS00059; ADH_ZINC; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 347 AA: 37569 MW; 46059B8AE2382DF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Hypothetical protein BH3213.
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100.0%; Pred. No. 3.8e+02;
tive 0; Mismatches 0;
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InterPro; IPR002085; Adh_zn_family.
InterPro; IPR000051; SAM_bind.
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PubMed=11572479;
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Best Local Similarity
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As Sawanabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,

Rawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,

Rawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,

Rawarabayasi Y., Sawada M., Horikawa H., Hosoyama A., Nagai Y.,

Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohiuku Y.,

Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi N.,

Roki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,

Rasuchi Y., Shizuya H., Kikuchi H.,

R. "Complete sequence and gene organization of the genome of a hyper-

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Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
Pyrococcus.
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                                                                                                                                     01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
348AA long hypothetical dehydrogenase.
                                                                             348 AA.
                                                                             PRT;
                                                                      PRELIMINARY;
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RESULT 15
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arch completed: February 14, 2003, 11:18:36 time: 12.5699 secs

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GenCore version 5.1.3
Copyright (c)'1993 - 2003 Compugen Ltd.
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using sw model OM protein - protein search, February 14, 2003, 11:04:17; Search time 46.0645 Seconds (without alignments) 49.176 Million cell updates/sec Run on:

US-09-701-001B-2 94 Title: Perfect score:

1 EIYPGSGSAYYNEMFKG 17 Sequence:

Scoring table:

908470 seqs, 133250620 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 ched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

| SIDS2/gcddata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS2/gcddata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Antibody 4H5 H cha	Murine CD4/CD34 re	Antibody 4H5 H cha	Murine derived pro	Antibody 4H5 H cha	Murine derived pro	Murine derived pro	Antibody 4H5 H cha	Antibody 4H5 L cha	Murine derived pro
QI	AAY59257	AAY51134	AAY 59262	AAY51139	AAY59266	AAY51143	AAY51145	AAY59264	AAY59265	AAY51141
3B	21	21	21	21	21	21	21	21	21	21
% Query Match Length DB ID	17	17	110	110	118	118	118	305	305	305
	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	94	94	94	94	94	94	94	94	94	94
Result No.	1	7	m	4	ស	9	7	8	6	10

305 21 AAY51142 119 2 AAY51264 121 18 AAW07437 123 16 AAR73017 113 18 AAW074591 248 20 AAY17965 248 20 AAY17965 242 20 AAY17965 251 20 AAY17953 252 20 AAY17953 251 20 AAY17953 251 20 AAY17962 251 20 AAY17962 251 20 AAY17963 251 20 AAY17963 251 20 AAY17963 251 20 AAY17963 251 20 AAW18267 91 21 AAW18267 91 22 AAG5886 91 22 AAG5886 91 22 AAG5886 91 23 AAW18277 92 21 AAW18277 93 20 AAW85911 94 23 ABP51797 95 20 AAW85915 96 22 AAG65867 97 20 AAW85916 98 20 AAW85916 99 20 AAW85916 90 21 AAW85916 91 22 AAG65867 92 20 AAW85917 93 20 AAW85917 94 20 AAW85917 95 20 AAW85917 96 21 AAW85917 97 20 AAW85917 98 21 AAW85917 99 20 AAW8591807 99 21 AAW8591807 90 21 AAW8591807 91 21 AAW8591807 92 21 AAG65867 93 AAW8591807	Murine derived pro Monoclonal antibod Anti-CD4 antibody Anti-DDA antibody Anti-DDA antibody Anti-DDA antibody Anti-DDA antibody Mouse scFV fragmen	44 antibody 81 heavy ch 81 heavy ch 81 heavy ch 10 acid sequ 1-prp antibo 1-prp antibo 1-prion prot 26 antibody 39 antibody 30 antibody 10 acid sequ 1-prp antibo 11 prp antibody 12 antibody 13 antibody 14 antibody 15 antibody 16 acid sequ 17 prp antibody 18 antibody 19 antibody 19 antibody 10 acid sequ 19 prp antibody 10 antibody 10 antibody
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ALIGNMENTS

Antibody 4H5 H chain variable region CDR2 fragment CD4 antigen; anti-human; antibody; 4H5; drug; CDR; complementarity determining region. AAY59257 standard; peptide; 17 AA (ASAH) ASAHI KASEI KOGYO KK 98JP-0163034. 98JP-0163034. 17-APR-2000 (first entry) JP11332563-A. 26-MAY-1998; 26-MAY-1998; 07-DEC-1999 AAY59257; Mus sp.

An antibody and the nucleic acid coding the antibody Claim 1; Page 14; 25pp; Japanese.

WPI; 2000-091351/08.

The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and

AA.

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The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the H chain variable region of the antibody 4H5.
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                                                                                                                                                                                                                                                                                CD4 antigen; anti-human; antibody; 4H5; drug.
                                                                                                                                                                                                                                           Antibody 4H5 H chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 15; 25pp; Japanese.
                                                                                                                      AAY59262 standard; protein; 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ASAH ) ASAHI KASEI KOGYO KK.
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      1 EIYPGSGSAYYNEMFKG 17
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Matches 17; Conserv
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AAY51139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of the motoryers from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived complementarity determining region CDR-2 protein fragment which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-JP02711. - PLT priority for Landens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells \,
application for drugs. It is highly safe in human dose. Sequences AAY59256-58 represent the complementarity determining region (CDR)-1, CDR-2 and CDR-3 fragments in the H chain variable region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine CD4/CD34 recognizing antibody heavy chain CDR-2 region #1.
                                                                                                                                                                                0;
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0
                                                                                                                                       100.0%; Score 94; DB 21; Length 17; llarity 100.0%; Pred. No. 5.1e-07; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 76; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                          AAY51134 standard; Protein; 17 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soka T, Morimoto I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ASAH ) ASAHI KASEI KOGYO KK.
(ASAH ) ASAHI MEDICAL CO LTD.
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98JP-0163023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDR-2; heavy chain; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                             4H5 respectively
                                                                                                                                                                                                                    1 EIYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                         EIYPGSGSAYYNEMFKG 17
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                                                                                                                                                       Local Similarity
es 17; Conserv
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nes 17; Conserv
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                                                                                                  17 AA;
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26-MAY-1998;
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AAY51134

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99WO-JP02711. - port print for index
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                                                                                                                                                                                                                 Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                         Gaps
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  Length 110;
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100.0%; Score 94; DB 21; 100.0%; Pred. No. 3.4e-06;
                     0; Mismatches
                                                                                                                                                                                              Murine derived protein fragment #1.
                                                                                                                         AAY51139 standard; Protein; 110 AA.
                                                                                                                                                                       (first entry)
                                            1 EIYPGSGSAYYNEMFKG 17
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us-09-701-001b-2; rag

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Gaps

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Indels

Length 118;

Score 94; .DB 21; Pred. No. 3.6e-06;

0; Mismatches

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Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                   Murine derived protein fragment #5.
                                                                                                                                                                                                AAY51143 standard; Protein; 118 AA.
                                     100.0%;
100.0%;
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                                                                                                               50 EIYPGSGSAYYNEMFKG 66
                                                                                              1 EIYPGSGSAYYNEMFKG 17
                                                                     Conservative
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Matches 17; Conserv
                                                      Local Similarity
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            118 AA;
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AAY51145
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                                                                                                                                                                                                                                       differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
                                                                                                                                                      Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                              This invention describes a novel device (I) for separating cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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100.0%; Pred. No. 3.4e-06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD4 antigen; anti-human; antibody; 4H5; drug.
                                                                                     Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 22; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY59266 standard; protein; 118 AA.
                                                                                                                                                                                                   Claim 22; Page 78; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody 4H5 H chain fragment
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                                                                                     Soka T, Morimoto I,
                                        (ASAH ) ASAHI KASEI KOGYO KK.
(ASAH ) ASAHI MEDICAL CO LTD.
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98JP-0159957.
98JP-0163023.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 EIYPGSGSAYYNEMFKG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EIYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Conservative
                                                                                                                WPI; 2000-086720/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 110 AA;
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                                                                                                                              N-PSDB; AAZ44203
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 25-MAY-1998;
               26-MAY-1998;
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                                                                                                                                                                                                                                                           Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells \,
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                                                                                                                 Soka T, Morimoto I, Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 94-95; 111pp; Japanese.
(ASAH ) ASAHI KASEI KOGYO KK.
(ASAH ) ASAHI MEDICAL CO LTD.
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Mus sp.

Ono M,

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The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the H chain sequence of the antibody 4H5.
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100.0%; Pred. No. 9.4e-06;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD4 antigen; anti-human; antibody; 4H5; drug.
                                                                                                                                                                                                                                                            Disclosure; Page 16-17; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 17-18; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY59265 standard; protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody 4H5 L chain sequence
                                                                                                                                    (ASAH ) ASAHI KASEI KOGYO KK.
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Matches 17; Conservative
                                                                                                                                                                    WPI; 2000-091351/08
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                                                                                                                                                                                                                                                                                                                                                                                        305 AA;
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                                                             26-MAY-1998;
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                                                                                                                                          Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of the production of new marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
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100.0%; Pred. No. 3.6e-06;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soka T, Morimoto I, Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 96-97; 111pp; Japanese.
   AA.
                                                                                                          Murine derived protein fragment #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY59264 standard; protein; 305 AA.
AAY51145 standard; Protein; 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibody 4H5 H chain sequence.
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(ASAH ) ASAHI MEDICAL CO LTD.
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                                                                       (first entry)
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st Local Similarity
tches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ44231
                                                                                                                                                                                                                                                   WO9961629-A1.
                                                                                                                                                                                                                                                                                                                          24-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                              25-MAY-1998;
26-MAY-1998;
                                                                       31-MAR-2000
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Seguence

AAY59264;

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RESULT 8

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Gaps

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Gaps

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hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lyaphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 94; DB 21;
100.0%; Pred. No. 9.4e-06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 22; Page 80-82; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY51142 standard; Protein; 305 AA.
                                                                                                                               AAY51141 standard; Protein; 305 AA.
                                                                                                                                                                                                                                           Murine derived protein fragment #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-JP02711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ono M, Soka T, Morimoto I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ASAH ) ASAHI KASEI KOGYO KK.
(ASAH ) ASAHI MEDICAL CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98JP-0159957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98JP-0163023.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000 (first entry)
                                                                                                                                                                                                       31-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EIYPGSGSAYYNEMFKG 17
                   72 EIYPGSGSAYYNEMFKG 88
1 EIYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-086720/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ44205
                                                                                                                                                                                                                                                                                                                                                                                             W09961629-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAY-1998;
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                                                                                                                                                                    AAY51141;
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AAY51142
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Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                     Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells \, \,^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Framework region; monoclonal antibody; variable domain; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody MAK CD4 heavy chain variable region peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 94; DB 21; 100.0%; Pred. No. 9.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                Soka T, Morimoto I, Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 22; Page 82-84; 111pp; Japanese.
            Murine derived protein fragment #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY51264 standard; peptide; 119 4
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                                                                                                                                                                                         99WO-JP02711.
                                                                                                                                                                                                                                                                    (ASAH ) ASAHI KASEI KOGYO KK. (ASAH ) ASAHI MEDICAL CO LTD.
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98JP-0163023.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EIYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunotherapy; MAK CD4
                                                                                                                                                                                                                                                                                                                                           WPI; 2000-086720/07.
N-PSDB; AAZ44206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 AA;
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                                                                                                                                WO9961629-A1.
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26-MAY-1998;
                                                                                                                                                              02-DEC-1999.
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                                                                                                      Mus sp.
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Gaps

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This sequence is the heavy chain variable region of a preferred anti-CD4 monoclonal antibody for use in the claimed synergistic composition. MAD WT 3.10 is deposited as clone 3.101/SB10 (ECACC 90090702). The anti-CD4 antibody is used with at least one anti-ILZR alpha or beta antibody. Individually the antibodies are strongly inhibiting and when used together their immunosuppressive properties are improved; they synergistically inhibit T-helper cell proliferation to effectively inhibit transplant rejection at low doses without significantly reducing the general immune response.
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heavy chain; variable region; anti-DNA; monoclonal; antibody; 4b2 group; hairpin; diagnosis; inflammatory glomerulonephritis; systemic luqus erythematosus; screening; treatment; prevention; SLE; disease; consensus; putative.
                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                          Length 137;
                                                                                                                                                                                                                                                      Score 88; DB 14; Length 13
Pred. No. 3.1e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-DNA antibody 4b2 group heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57..98
/label= framework_III
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/label= framework_II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= framework_I
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW07437 standard; Protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= J_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= CDR_III
1111..121
               Claim 5; Page 12; 18pp; German.
                                                                                                                                                                                                                                                                                        0;
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/label= CDR_II
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/label= CDR_I
                                                                                                                                                                                                                                                        93.68;
94.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                        1 EIYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                                                                        68 EIYPGSGSAYYNEKFKG 84
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99..110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-011854/01.
                                                                                                                                                                                                                                                                     Local Similarity
Les 16; Conserv
                                                                                                                                                                                                                          137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT43806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9636361-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-NOV-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW07437;
                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
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                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                    This invention describes novel peptides derived from a framework region of the variable domain of an antibody for detection, immunotherapy or for scintigraphs. The peptides of the invention are used in a method to detect analytes in a sample by eliminating interference in the sample. AAY51254-Y51267 represent peptides derived from the framework regions of the variable domain of an antibody which are used to illustrate the
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunosuppression; tissue transplantation; graft, H chain; V region;
I-helper cell inhibition; transplant rejection; MAb;
interleukin-2 receptor.
                                                                                                                                         Suppressor peptides derived from antibodies for use in immunoassays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synergistic antibody compsn. for use as immunosuppressant - comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R alpha- or anti-IL2R beta antibodies
                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                     Length 119;
                                                                                                                                                                                                                                                                                                                                                                  Score 88; DB 21; Length 11
Pred. No. 2.7e-05;
Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-CD4 antibody MT 3.10 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scheuer W, Weidle U;
                                                                           Lenz H, Praast G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR32124 standard; Protein; 137 AA.
                                                                                                                                                                         Disclosure; Page 16; 20pp; German.
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/label- signal
19..125
/label= variable
126..137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                           (HOFF ) ROCHE DIAGNOSTICS GMBH.
                                                                                                                                                                                                                                                                                                                                                                   93.6%;
94.1%;
           98DE-1028466.
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91DE-4143214.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= J3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIIIIIIIIIII III
EIYPGSGSAYYNEKFKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EIYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                           Moessner E,
                                                                                                                                                                                                                                                                                                     method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1993-037582/05.
                                                                                                         WPI; 2000-107255/10.
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                     119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ36610.
           26-JUN-1998;
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30-DEC-1991;
                                                                           Nussbaum S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-DEC-1991;
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                                                                                                                                                                                                                                                                                                                                       Seguence
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AAR32124;

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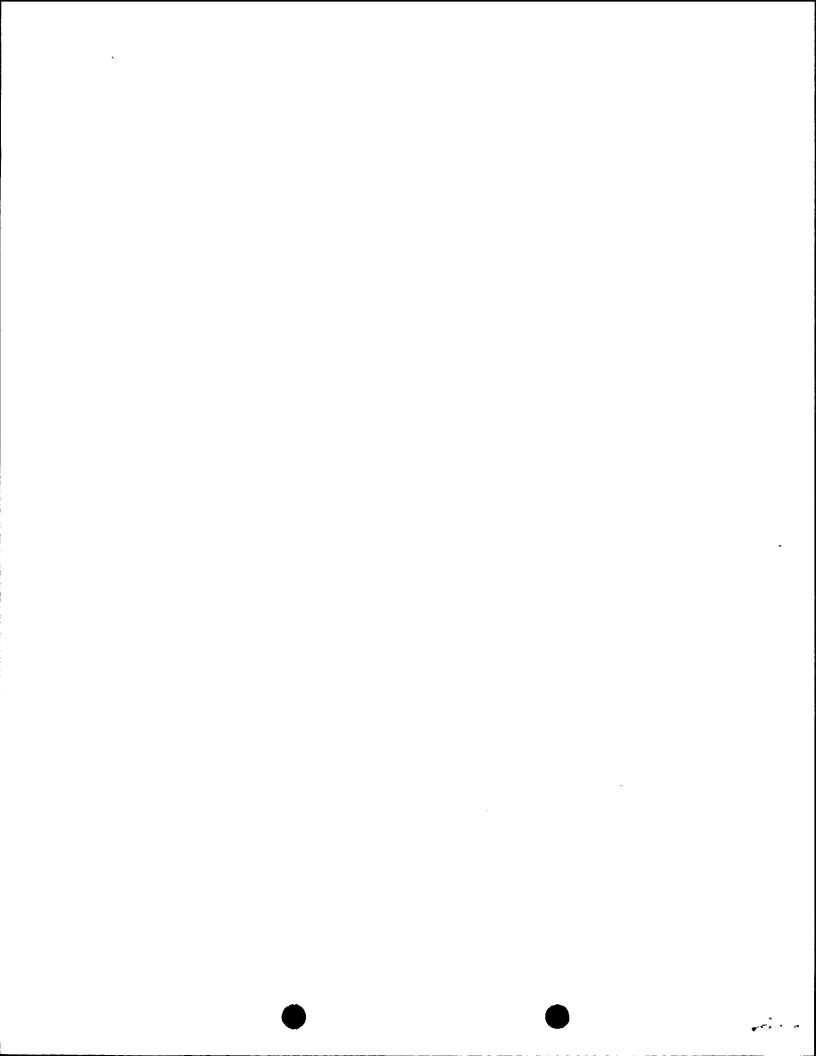
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RESULT 13 AAR3212 Peptide Region Region

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Gaps
                                                                                 The present sequence is the heavy chain variable region of the group 4b2 putative consensus anti-DNA monoclonal antibody (MAb), which has a high affinity for single stranded DNA, low or no affinity for double stranded DNA and specifically binds a DNA hairph. The MAb can be used diagnose disorders associated with the pathological complexation of DNA, e.g. inflammatory glomerulonephritis and systemic lupus erythematosus. It can also be
Anti-DNA antibody which specifically binds DNA hairpin - useful to develop prods. for diagnosis and treatment of disorders, e.g. glomerulonephritis or systemic lupus erythematosus
                                                                                                                                                                                   used to generate reagents to screen for pharmaceutical agents, and treat and/or prevent an above disorder.
The sequence was derived by aligning homologous anti-DNA MAD, whose sequences have been published as well as several MAD of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single chain antibody, antibody, epidermal growth factor receptor; EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment; phage antibody library.
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0
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                                                                                                                                                                                                                                                                                                 86.2%; Score 81; DB 18; Length 121; 82.4%; Pred. No. 0.00028; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                             other specificities obtained from a database search
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113..123
/label= Framework region 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36..49
/label= Framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR79877 standard; Protein; 123 AA.
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                                                        Example; Fig 9; 102pp; English.
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/label= CDR2.
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/label= CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31..35
/label= CDR1.
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used for diagnosis of tumours and assessment of tumour growth in vitro and in vivo. They may also be used in a pharmaceutical compostion for the therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and fragments are derived from mice but are humanised so as to cause minimum reaction against them. They are produced using the phage antibody library. (See AAT04011-T04026 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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81.2%; Pred. No. 0.0015;
.ive 1; Mismatches 2; Indels
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                Guessow
Rosell E;
Adan J, Ansell KH, Bendig MM, Blasco F,
Kettleborough AC, Mitjans F, Piulats J,
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nes 13; Conserv
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                                                  February 14, 2003, 11:13:07; Search time 15.3548 Seconds (without alignments) 32.575 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-881-037-64

US-08-881-037-65

US-08-713-939A-70

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US-09-550-374-70

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US-09-550-374-70

US-09-550-374-70

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-08-713-939A-84
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                                                                                                                                                    262574 seqs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries
                                   - protein search, using sw model
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94
1 EIYPGSGSAYYNEMFKG 17
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GENERAL INCORNATION:
APPLICANT: Praast, Gerald
APPLICANT: Praast, Gerald
APPLICANT: Nussbaum, Sabine
APPLICANT: Nussbaum, Sabine
APPLICANT: Lenz, Helmut
TITLE OF INVENTION: BEDUCTION OF INTERFERENCE OF IMMUNOASSAYS BY SUBSTANCES
TITLE OF INVENTION: DERIVED FROM THE FRAMEWORK REGIONS OF ANTIBODIES
FILE REFERENCE: BMID 9928 4897/00/US-IM
CURRENT APPLICATION NUMBER: US/09/344,587
CURRENT PILLING DATE: 1999-06-25
EARLIER PILLING DATE: 1990-06-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.1
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         US-09-550-374-83
US-08-713-939A-68
US-08-713-939A-76
US-08-713-939A-77
US-09-036-579-76
US-09-036-579-76
US-09-550-374-68
US-09-550-374-68
US-09-550-374-76
US-09-550-374-76
US-08-68-83-66-2
US-08-767-128-20
US-08-767-128-20
US-08-458-516-10
US-08-458-516-10
US-08-458-516-10
US-08-458-516-10
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Pred. No. 7e-06;
0; Mismatches
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Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                      US-09-344-587-11
; Sequence 11, Application US/09344587
; Patent No. 6331402
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94.1%;
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Best Local Similarity 94.1
Matches 16; Conservative
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ZIP: 94304-1018
COMPUTER READABLE FORM:
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CITY: Palo Alto
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TYPE: PRT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18 May-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 65, Application US/08881037 Patent No. 6080588 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 20:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
                      INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                  1 EIYPGSGSAYYNEMFKG 17
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STRANDEDNESS: single
                                                                                                                                  linear
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Best Local Similarity
Matches 13; Conserva
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ZIP: 94304-1018
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nes 13; Conserv
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US-08-881-037-18
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US-08-881-037-65
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    TELEX:
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                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTONREY/AGENT INFORMATION:
NAME: KONSKI, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1800
TELECOMMUNICATION 1800
TELECOMMUNICATION 1800
TELECOMMUNICATION 1800
TELECOMMUNICATION 1800
TELEFRAX: (650) 813-5600
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ZIP: 94304-1018
COUNTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203442110710
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APPLICATION NUMBER: US 08/443,540
FILING DATE: 18 MAY-1995
CLASSIFICATION: 530
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: KOBSK, ANCIDECTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 2034
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                               64:
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 EIYPGSGNTYYNEKFKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EIYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                                                                                                                                         TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity
Matches 14; Conserv
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TOPOLOGY:
US-08-881-037-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                          CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.3
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EIYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bozicevic, Karl
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIFE. SIRANDEDNESS: SIR
                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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US-08-713-939A-78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 70. Application US/08713939A
Patent No. 5846533
CENERAL INFORMATION:
APPLICANT: Pursiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
                                                     GENERAL INFORMATION:
APPLICANT: RYDak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Miodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                       ZIP: 94111-3834

ZIP: 94111-3834

COMPUTER REAGABLE FORM:
COMPUTER: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
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APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER: US/08/875,811
19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFRAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
              Sequence 57, Application US/08875811
Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Faris, Susan K. REGISTRATION NUMBER: 41,739
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168 DIYPGSDNTYYNEKFKG 184
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Best Local Similarity 70.6
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                             USA
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US-08-713-939A-70
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US-08-875-811-57
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COMPUTER: INA COMPATIBLE

CLASSITION WINDER:

FULLING DATE:

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TELEFAX: 415-854-0875

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STRANDEDNESS:
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     RESULT 9
US-09-036-579-78
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US-09-550-374-70
                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                     CITY: 1
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                                                                                                                                                            Score 68; DB 2; Length 91;
Pred. No. 0.0042;
2; Mismatches 3; Indels
                                                                                                                                                               Length 91;
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                                                                                                                                                                                                                                                                                                                                                quence 70, Application US/09036579
detent No. 6290954
dent No. 6290954
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06510/059001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,579
FILING DATE:
CLASSIFFICATION:
PRIOR APPLICATION UNBER: 08/713,939
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIR: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28,807
                                                                                                                                                          72.3%;
70.6%;
                  SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
                                                                                                                                                        Query Match 72.39
Best Local Similarity 70.69
Matches 12; Conservative
                                                                                                                                                                                                                                                  24 EIWPRSGNTYYNEKFKG 40
                                                                                                                                                                                                                              1 EIYPGSGSAYYNEMFKG 17
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INFORMATION FOR SEQ ID NO:
                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Bozicevic, Karl
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-854-0875
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; MOLECULE TYPE: peptide
US-09-036-579-70
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                         US-08-713-939A-78
                                                                                                                                                                                                                                                                                                                   RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                       GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTON: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTON: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06510/059001
                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FRASTSEQ Version 2.0
SOFTWARE: APPLICATION DATA:
APPLICATION NUMBER: US/09/036,579
                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Fish & Richardson P.C. STREET: 2200 Sand Hill Road
Sequence 78, Application US/09036579 Patent No. 6290954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,939
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 70, Application US/09550374; Patent No. 6372214; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BOZICEVIC, KATI
REGISTRATION NUMBER: 28,807
REFERENCE/POCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFRAX: 415-854-0875
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 91 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1|:| ||: |||| ||| 24 EIWPRSGNIYYNEKFKG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EIYPGSGSAYYNEMFKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-036-579-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Menlo Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.3%; Score 68; DB 4; Length 91; 70.6%; Pred. No. 0.0042; Live 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 79, Application US/08713939A
Sequence 79, Application US/08713939A
Patent No. 5846533
Patent No. 5846333
Patent No. 5846533
Patent No. 5846333
Patent No. 58
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70.6%; Pred. No. 0.0043;
tive 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
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13-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FASTSEO Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/713,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EIYPGSGSAYYNEMFKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 13-SEP-19
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION UMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
TELEPHONE: 415-854-5277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1|:| ||: |||| |||
24 EIWPRSGNTYYNEKFKG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 72.33
Best Local Similarity 70.63
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EIYPGSGSAYYNEMFKG 17
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                                                                                                                  INFORMATION FOR SEQ ID NO:
                                          TELEFAX: 415-854-0875
                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-09-550-374-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Menlo Park
                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Menl
STATE: CA
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US-08-713-939A-79
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
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APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
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REGISTRATION UNBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06510/059001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/550,374
                                                                                                                                                                                                                    SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/550,374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/036,579
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 78, Application US/09550374 Patent No. 6372214 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIETCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/036,579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BOZICEVIC, Karl
REGISTRATION NUMBER: 28,807
REFRENCE/DOCKET NUMBER: 0651
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-6277
TELEPHAX: 415-854-0875
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MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
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                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
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Best Local Similarity 70.6
Watches 12; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94025
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COUNTRY:
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Patent No. 6290954

GENERAL INFORMATION:

APPLICANT: Williamson, R. Anthony
APPLICANT: Button, Dennis R.

TTLE OF INVENTION:

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 2200 Sand Hill Road

CITY: Menlo Park
                                                                                          Sequence 85, Application US/08713939A
Patent No. 5846533
GENERAL INFORMATION:
APPLICANT: Fursiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TILLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.3%; Score 68; DB 2; Length 92; 70.6%; Pred. No. 0.0043; tive 2; Mismatches 3; Indels
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13-SEP-1996
                                                                                                                                                                                                                                                                    ADDRESSEE: Fish & Richardson P.C. STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FSS.ESD Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,93**
FILING DATE: 13-SFPD-1**
CLARCETION OF THE COMPANY OF THE COMP
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
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25 EIWPRSGNTYYNEKFKG 41
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LENGTH: 92 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bozicevic, Karl
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-713-939A-85
                                                                                                                                                                                                                                                                                                          Menlo Park
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                                                                                                                                                                                                                                                                                                                                CA
                                                      RESULT 13
US-08-713-939A-85
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US-09-036-579-79
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                                                                              OPPRATING SYSTEM: DOS
SOFTWARE: FASCED Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION NOMBER: US/09/036,579
APPLICATION NUMBER: US/09/036,579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fish & Richardson P.C. STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPE
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,939
FILLING DATE: 13-SEP-1996
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 85, Application US/09036579; Patent No. 6290954; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    NAME: BOZICEVIC, KATI
REGISTRATION NUMBER: 28,807
REFRENCE/POCKET NUMBER: 0651
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
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APPLICATION NUMBER: 08/713,939
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                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.3°
Best Local Similarity 70.6°
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EIYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 EIWPRSGNTYYNEKFKG 41
               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-036-579-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 92 amino TYPE: amino acid STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Menlo Park
                                                                                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: CLASSIFICATION:
94025
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TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-884-5277

TELEFAX: 415-884-0875

TELEFAX: 415-884-0875

TELEFAX: 415-884-0875

TELEFAX: 415-884-0875

TELEX:

INFORMATION FOR SEQ ID NO: 85:

SEQUENCE CHARACTERISTICS:

TYPE: amino acids

TYPE:
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February 14, 2003, 11:15:53; Search time 9.87097 Seconds (without alignments) 44.001 Million cell updates/sec
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140259 seqs, 25548876 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                              - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                      1 EIYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                      US-09-701-001B-2
94
                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                    OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ched:
                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

		Description	Sequence 70, Appl	Sequence 78, Appl	Sequence 79, Appl	Sequence 85, Appl	Sequence 86, Appl	Sequence 82, Appl	Sequence 84, Appl	Seguence 83, Appl	Sequence 68, Appl	Sequence 76, Appl	Sequence 77, Appl	Sequence 71, Appl	Sequence 31, Appl	Sequence 15, Appl	Sequence 4, Appli	Sequence 75, Appl	Sequence 69, Appl	Sequence 31, Appl	Sequence 71, Appl
SUMMARIES		QI	US-09-943-906-70	US-09-943-906-78	US-09-943-906-79	US-09-943-906-85	US-09-943-906-86	US-09-943-906-82	US-09-943-906-84	US-09-943-906-83	US-09-943-906-68	US-09-943-906-76	US-09-943-906-77	US-09-144-886-71	US-08-779-784-31	US-09-861-294-15	US-09-861-294-4	US-09-943-906-75	US-09-943-906-69	US-09-956-206A-31	US-09-943-906-71
		gth DB	91 10	91 10	92 10	92 10	95 10	101 10	103 10	108 10	114 10	114 10	114 10	117 9	138 1	17 10	153 10	105 10	114 10	31 9	91 10
	% Ouerv	Match Length	72.3	72.3	72.3	72.3	72.3	72.3	72.3	72.3	72.3	72.3	72.3	70.2	70.2	69.1	69.1	68.1	68.1	0.99	0.99
		Score	89	68	89	89	68	99	89	89	99	68	68	99	99	65	65	64	64	62	62
)	Result	No.	-	7	3	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19

NAME: Bozicevic, Karl REGISTRATION NUMBER: 28,807 REFERENCE/DOCKET NUMBER: 06510/059001

TELECOMMUNICATION INFORMATION: TELEPHONE: 415-854-5277 TELEFAX: 415-854-0875

LENGTH: 91 amino acids STRANDEDNESS: single

TYPE: amino acid

INFORMATION FOR SEQ ID NO: 70: SEQUENCE CHARACTERISTICS: TELEX: <Unknown>

Sequence 81, Sequence 80, Sequence 1, A Sequence 1, A Sequence 6, Ap equence 72, A Sequence 86, Sequence 87, Sequence 87, Sequence 85, Sequence 95,	Sequence 49, Appl Sequence 46, Appl Sequence 51, Appl Sequence 55, Appl Sequence 9, Appl Sequence 13, Appl Sequence 8, Appli Sequence 8, Appli Sequence 5, Appli Sequence 5, Appli	Pre	
US-09-943-906-81 US-09-943-906-80 US-09-93-906-80 US-09-839-447A-1 US-09-839-447A-1 US-09-905-928-6 US-09-144-886-72 US-09-825-012-38 US-09-825-012-38 US-09-825-012-80 US-09-825-012-95 US-09-825-012-95 US-09-825-012-95 US-09-825-012-95 US-09-825-012-95 US-09-825-012-95 US-09-825-012-95 US-09-825-012-95 US-09-825-012-95 US-09-825-012-95	US-09-825-012-49 US-09-825-012-46 US-09-825-012-51 US-09-825-012-55 US-09-839-447A-9 US-10-146-305-8 US-10-146-305-8 US-10-141-908-2 US-10-141-908-5	ony SPECIFIC FOR NATIVE Son P.C.	TEM: DOS tSEQ Version 2.0 tSEQ Version 2.0 UMBER: US/09/943,906 30-Aug-2001 N: CUNKNOWN> UMBER: 09/550,374 UMBER: 09/550,374 CUNKNOWN> CURNOWN> CURNOWNSION:
62 66.0 91 10 62 66.0 99 10 62 66.0 139 10 62 66.0 139 10 60 63.8 140 9 59 62.8 517 10 59 62.8 519 10 59 62.8 519 10 59 62.8 519 10 59 62.8 521 10 59 62.8 521 10 59 62.8 521 10 59 62.8 521 10 59 62.8 529 10 59 62.8 529 10	62.8 730 1 9 62.8 731 1 9 62.8 731 1 9 62.8 740 1 9 62.8 741 1 8 61.7 20 1 7 60.6 138 9 6 59.6 118 9	1 1943-906-70 ence 70, Application US, or US20020150571A1 NERAL INFORMATION: APPLICANT: PTUSINER, WILLIAMSON BUILDE, OF INVENTION: DESCRESSONERS ADDRES A	OPERATING SYSTEM: DOS SOFTWARE: FASTSEQ VERSION CURRENT APPLICATION NUMBER: US/09 FILING DATE: 30-Aug-2001 CRASSIFICATION NUMBER: US/09 PRIOR APPLICATION NUMBER: U9/55 APPLICATION NUMBER: U9/55 TILING DATE: CURROWN> ATTORNEY/AGENT INFORMATION: NAME: BOZICCHION:
3 3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	8 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	RESULT 1 US-09-91 Sequent Patent GENET CENET CEN	

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Patent No. US20020150571A1 GENERAL INFORMATION:
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Williamson, R. Anthony
Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PLP
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.3%; Score 68; DB 10; Length 91; 70.6%; Pred. No. 0.0021; tive 2; Mismatches 3; Indels
                                                                                                           72.3%; Score 68; DB 10; Length 91; 70.6%; Pred. No. 0.0021; Live 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/550,374
FILING DATE: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-0877
TELEFAX: 415-854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,906
; TOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 70: US-09-943-906-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 78:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       Sequence 78, Application US/09943906
Patent No. US20020150571A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 78:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                     ||:| ||: |||| |||
24 EIWPRSGNTYYNEKFKG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Menlo Park
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 EIWPRSGNTYYNEKFKG 40
                                                                                                              Query Match 72.3
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                             1 EIYPGSGSAYYNEMFKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 94025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity
Matches 12; Conserv
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US-09-943-906-78
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US-09-943-906-79; Sequence 79, Application US/09943906

RESULT 3

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Gaps
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Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SECUENCES: 86
CORRESPONDENCE ADDRESS:
APPLICANT: Prusiner, Stanley B.
Williamson, R. Anthony
Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.3%; Score 68; DB 10; Length 92; 70.6%; Pred. No. 0.0021; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,906
FILING DATE: 30-Aug-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                   ADDRESSEE: Fish & Richardson P.C. STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Fish & Richardson P.C. STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 79:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/550,374
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,807
                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: ISM COMPATIBLE
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTESEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 85, Application US/09943906; Patent No. US20020150571A1
GENERAL INFORMATION: APPLICANT: Prusiner, Stanley B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 92 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 79: SEQUENCE CHARACTERISTICS:
                                                                                           NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                     CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EIYPGSGSAYYNEMFKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: <Unknown>
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                                                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 94025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U ZIP: 94025
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                                                                                                                                                                                                            STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-943-906-79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Prusiner, Stanley B.
Williamson, R. Anthony
Burton, Dennis R.
TITLE OF INVENTIONS: 86
CORRESPONDENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                        Length 95;
                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
                                                                                                                                                                                          72.3%; Score 68; DB 10; 70.6%; Pred. No. 0.0022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,906
FILING DATE: 30-Aug-2001
                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Fish & Richardson P.C. STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 82:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/550,374
                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-943-906-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 28,807
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 82, Application US/09943906
Patent No. US20020150571A1
GENERAL INFORMATION:
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NAME: BOZICEVIC, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diskette
                  SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 82:
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INFORMATION FOR SEQ ID NO: 86:
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MEDIUM TYPE: Diske
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Menlo Park
                                                                                                                                                                                                                                                                           1 EIYPGSGSAYYNEMFKG 17
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28 EIWPRSGNTYYNEKFKG 44
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Matches 12; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94025
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Williamson, R. Anthony
Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PIP
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.3%; Score 68; DB 10; Length 92; 70.6%; Pred. No. 0.0021;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
                                                                                                                                                                     FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, KATI
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-884-5277
TELEFAX: 415-884-0875
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FILING DATE: 30-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Fish & Richardson P.C. STREET: 2200 Sand Hill Road
          OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,906
FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 85:
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PILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 09/550,374
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REGISTRATION NUMBER: 28,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                TELEX: <URNOWN>
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
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MEDIUM TYPE: Diske
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Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PRP
NUMBER OF SQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.3%; Score 68; DB 10; Length 103; 70.6%; Pred. No. 0.0024; Live 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Prusiner, Stanley B.
Williamson, R. Anthony
Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE Prp
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,906
                                                                                                                                                                                                                      ADDRESSEE: Fish & Richardson P.C. STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Fish & Richardson P.C. STREET: 2200 Sand Hill Road CITY: Menlo Park
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 84:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/550,374
                                                                                              APPLICANT: Prusiner, Stanley B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
                                   Sequence 84, Application US/09943906
Patent No. US20020150571A1
GENERAL INFORMATION:
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Patent No. US20020150571A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 103 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: CURKNOWN>
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  ZIP: 94025
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                         CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                              STATE: CA
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              US-09-943-906-84
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RESULT 7
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Patent No. US20020150571A1
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
Milliamson, R. Anthony
Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, KATI
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-844-5277
TELEPHONE: 415-854-0875
                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,906
FILING DATE: 30-Aug-2001
CLASSIFICATION: <union-controlly.
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Fish & Richardson P.C. STREET: 2200 Sand Hill Road
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 83;
                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/550,374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/550,374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 108 amino acids
                 ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                       FILING DATE: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 70.69
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EIYPGSGSAYYNEMFKG 17
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COUNTRY: U.S.A.
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Gaps
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                                                                                                                                                                                                                                   APPLICANT: Prusiner, Stanley B.
Milliamson, R. Anthony
Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
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  Indels
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TELECOMMUNICATION INFORMATION:
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SOFTWARE: FastSED Version 2.0

CURRENT APPLICATION DATA: US/09/943,906

FILING DATE: 30-Aug-2001

CLASSIPICATION: «URKNOWN»

PRIOR APPLICATION NUMBER: 09/550,374
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    2; Mismatches
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ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 77:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, Karl
REGISTRATION NUMBER: 28,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 71, Application US/09144886 Patent No. US20020155114A1
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                                                                                                                                                                      Sequence 77, Application US/09943906 Patent No. US20020150571A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 114 amino acids
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 77:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EIYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||:| ||: |||| |||
47 EIWPRSGNTYYNEKFKG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Menlo Park
                                                               47 EIWPRSGNTYYNEKFKG 63
                                           1 EIYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
      Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-09-144-886-71
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                                                                                                                                                             US-09-943-906-77
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                                                                                                                                               RESULT 11
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                                                                                                                                                                                                                                                                                                       Query Match 72.3%; Score 68; DB 10; Length 114; Best Local Similarity 70.6%; Pred. No. 0.0026; Matches 1: Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Prusiner, Stanley B.
Williamson, R. Anthony
Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 68; DB 10;
Pred. No. 0.0026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIG, KARIL
REGISTRATION NUMBER: 28,807
REFERENCE/TOKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-864-5277
TELEPAX: 415-864-0875
              REFERENCE/DOCKET NUMBER: 06510/059001
                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/09/943,906
FILING DATE: 30-Aug-2001
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Fish & Richardson P.C. STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-09-943-906-76
                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-943-906-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/550,374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 76, Application US/09943906
Patent No. US20020150571A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 114 amino acids
                                                                                                                                                     LENGTH: 114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 76:
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70.6%;
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                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                            INFORMATION FOR SEQ ID NO: 68: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                           Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                       1 EIYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                                                                                  12; Conservative
                                                                                              TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-943-906-76
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us-09-701-001b-2.rapb

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; ORGANISM: Mus musculus US-08-779-784-31
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US-09-861-294-15
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LENGIH: 17
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APPLICANT: Miller, David J.
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
CORRESPONDENCE: 37
ADDRESSEE: David A T.-.
STREEP.
                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone OTHER INFORMATION: 1G5 region VH epitope 3
                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                          70.2%; Score 66; DB 9; Length 117; 75.0%; Pred. No. 0.0052; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
RIOR APPLICATION NUMBER: US 08/520,84
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
AND ARTHUR DATE: APPLICATION NUMBER: US 08/236,520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1199-1-001 CIPA
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PAtentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31, Application US/08779784 Patent No. US20020164325A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 11.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 138 amino acids
amino acid
                                                                                                                                                                                                                                                                     Query Match 10.28
Best Local Similarity 75.09
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Floor
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-779-784-31
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                                                                                   SEQ ID NO 71
LENGTH: 117
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: TOWNES BEARING HMFG AND CEA ANTIGENS
FILE REFERENCE: 304142000620
CURRENT APPLICATION NUMBER: US/09/861;294
CURRENT FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/049,540
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1998-06-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-09-861-294-4
Sequence 4, Application US/09861294
Sequence 4, Application US/09861294
Sequence 4, Sequence 5, Sequence 7, Sequence 7, Sequence 7, Sequence 7, Sequence 7, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 9, Sequence 8, Sequence 9, Sequ
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              70.2%; Score 66; DB 1; Length 138; 75.0%; Pred. No. 0.0061; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.1%; Score 65; DB 10; Length 17; 62.5%; Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/09861294; Patent No. US20020098190a1; GENERAL INFORMATION: APPLICANT: Malaya CHATTERJEE; APPLICANT: Kenneth A. FOON
Query Match
Best Local Similarity 75.08
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                     70 IYPGDGSTKYNEKFKG 85
                                                                                                                                                                                                           2 IYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 IYPGSGSAYYNEMFKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Mus musculus
US-09-861-294-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus
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; LOCATION: (1)...(19)
US-09-861-294-4
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, 0 0; Gaps Best Local Similarity 62.5%; Pred. No. 0.0094; Matches 10; Conservative 3; Mismatches 3; Indels

2 IYPGSGSAYYNEMFKG 17 |:||:| |||: ||| 70 IFPGNGDTYYNQKFKG 85

Search completed: February 14, 2003, 11:21:29
Job time : 9.87097 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 14, 2003, 11:12:02; Search time 17 Seconds (without alignments) 96.134 Million cell updates/sec Run on:

US-09-701-001B-2 94 1 EIYPGSGSAYYNEMFKG 17 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283224 seqs, 96134422 residues :paq:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	heavy chain	heavy	heavy chain	heavy cha	gamma-2b cha	heavy	Ig heavy chain V r	heavy cha	heavy	heavy	heavy cha	kappa cha	heavy	heavy	heavy	heavy chain V	heavy chain V	gamma cha	gamma-2a chain	heavy chain	heavy chain	heavy chain	heavy chain V-	heavy chain V	heavy	gamma cha	heavy cha	Ig heavy chain V r	Iq heavy chain V r	•
	QI	S19964	PH1227	519966	PH1000	501321	pH1165	G32513	G37262	550Hd	E30562	S19969	H28833	666UHd	PH0997	8660Hd	C30562	D30562	538950	\$40295	526466	HVMSA1	F29380	926608	PD0008	PH1159	\$42185	PH1002	DH1001	A5/378	ה ה
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	ength I	119	137	117	110	475	90	0.4	9.5	111	110	121	129	107	100	111	110	119	246	446	104	117	137	120	120	06	ν δ	106	001	115	777
æ	Query Match Length	93.6		0.70	, c	23.0	0.0	77.7	76.6	9.9	, r	73.5	 	71.3	71.3	71.3	71.3	71.5	71.3	71.5		10.7	70.2	. 5 4	1.09	2 2	. 69	1.00		9 0	1.00
	Score	α α	0 0	000	700	707	2 7	7.0		7 / 2	7 - 6	4 0	0 0	00	19	10	0 4	70	70	70	2	9 9	9 9	9 4	ט ע ע	0 4	7 4	† *	* 0	4.	P4
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0; Gaps

Query Match
93.6%; Score 88; DB 2; Length 137;
Best Local Similarity 94.1%; Pred. No. 1.1e-06;
Matches 16; Conservative 0; Mismatches 1; Indels

Ig heavy chain pre Ig heavy chain V r Ig heavy chain V r Ig heavy chain (an Ig heavy chain V r monoclonal antibod Ig gamma chain V r Ig heavy chain V r Ig heavy chain V r r
899 772 772 772 772 777 777 778 778 179 181 180 880 880
\$03289 \$28572 \$28814 \$26700 \$06825 \$7217 \$42177 \$42177 \$42177 \$42178 \$42186
000000000000000000
117 76 116 115 122 214 94 94 95 97 101 101 102 137 469
668.1 666.0 664.9 664.9 663.8 663.8 663.8 663.8 663.8 663.8
4226 60122 600 600 600 600 600
330 330 330 330 330 330 330 444 445 445 445 445 445 445 445 445 44

ALIGNMENTS

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Ig heavy chain V region (clone 26F.1) - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Species: 30-680-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C.Accession: PH1165
R.Schittek, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A.Title: Natural occurrence and origin of sometically mutated memory B cells in mice.
A.Reference number: PH1105; MUID:92364545; PMID:1500855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Igheavy chain V region (BXW14) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21 May-1990 #sequence_revision 31-Dec-1990 #text_change 16-Aug-1996
C;Accession: G32513
C;Accession: G32514
J. Ciln. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization a A;Accession: G32513
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
A;Molecule type: mRNA
A;Residues: 1-475 <DE1>
A;Cross-references: EMBL:X13188; NID:951780; PIDN:CAA31580.1; PID:951781
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;15-96/Domain: immunoglobulin homology <IMM>
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81.2%; Pred. No. 5.9e-05;
tive 1; Mismatches 2; Indels
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Pred. No. 0.00017;
                                                                                                                                                                  C. Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F:159-223/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 76.5
Matches 13; Conservative
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es 13; Conserv
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Best Local Similarity
Matches 13; Conserv.
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A; Residues: 1-96 <SCH>
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A; Residues: 1-94 <KOF>
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PH1165
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G37262
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C;Species: Mus musculus (house mouse)
C;Date: 30.Sep-1993 #sequence_revision 30.Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1000
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Tille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B A;Reference number: PH0971; MUID:92381444; PMID:1512540
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19 gamma-2b chain precursor - mouse
19 gamma-2b chain precursor - mouse
25 Species: Mus musculus (house mouse)
25 Accession: 801321

C:Accession: $01321

R:de Weale, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.

Bur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed
A:Accession: $01321

A:Accession: $01321
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Cispeciaes, Mis musculus (house mouse)
Cispate: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 16-Aug-1996
Rivelssenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
A; Description: Structural characterization of CD4 mAb.
A; Reference number: S19963
A; Status: preliminary
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'ywords: heterotetramer; immunoglobulin
15-98/Domain: immunoglobulin homology <IMM>
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A/Experimental sou
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82.4%; Pred. No. 1.1e-05;
tive 1; Mismatches 2; Indels
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88.2%; Pred. No. 8.1e-06;
tive 0; Mismatches 2; Indels
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A.Cross-references: EMBL:X65085
                                      68 EIYPGSGSAYYNEKFKG 84
   1 EIYPGSGSAYYNEMFKG 17
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Best Local Similarity
Matches 15; Conserv
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A: Residues: 1-117 <WEI>
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J. Immunol. 141, 779-784, 1988
A;Title: Allogeneic manipulation of the GAT idiotypic cascade. Immunization of C57BL/A;Reference number: A92827; MUID:88285674; PMID:3135311
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH0999
B;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Tille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective A;Teference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH0999
A;Status: nucleic acid sequence not shown
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C;Species: Mus musculus (house mouse)
C;Date: 30-5ep-1999 #sequence_revision 30-Sep-1989 #text_change 09-May-1997
C;Accession: H28833
R;Corbet, S; Hirn, M; Roth, C.; Theze, J.; Fougereau, M.; Schiff, C.
                                                                                                                                                                                                                                                                              Ig heavy chain V region (M-T413) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-Jul-1999
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                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                  C;Accession: S19969
R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P. submitted to the EMBL Data Library, March 1992
A;Description: Structural characterization of CD4 mAb.
                                     Indels
Pred. No. 0.00046;
1. Mismatches 3;
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Pred. No. 0.00098;
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                                     1; Mismatches
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A,Residues: 1-67 COOR>
C;Superfamily: immunoglobulin V region; imm
C;Keywords: heterotetramer; immunoglobulin
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81.2%;
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75.0%;
           76.5%;
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Best Local Similarity 81.23
Matches 13; Conservative
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Best Local Similarity 75.0
Matches 12; Conservative
           Best Local Similarity 76.5
Matches 13; Conservative
                                                                                            1 EIYPGSGSAYYNEMFKG 17
                                                                                                                                                 50 EIFPGSGSTKYNEKFKG 66
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A; Accession: S19969
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A; Residues: 1-121 <WEI>
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C;Species: Mus musculus (house mouse)
C;Species: 33-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C;Accession: E30562
R;Sikder. S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.I.
J. Immunol. 142, 888-893, 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bian Reference number: A30562; MUID:89110066; PMID:2464031
        Ig heavy chain V region (14D2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 16-Aug-1996
C;Accession: G37262
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
B;Goshorn, Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same antigen A;Reference number: A38601; MUID:91115823; PMID:1703527
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R;Tillnan, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992

A;Title: Both 1gd and 1gG anti-DNA antibodies are the products of clonally selective B A;Reference number: PH0971; MUID:92381444; PMID:1512540
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
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A;Residues: 1-111 <TIL>
A;Residues: 1-111 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                      A)Cross-references: GB:M57993
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-84/Domain: immunoglobulin homology <IMM>
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Pred. No. 0.00025;
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A; Residues: 1-119 <SIK>
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75.5%; Score 71; DB 2; Length 119;

Query Match

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Job time : 17 secs
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C; Species: Mus musculus (house mouse)
C; Species: Musculus (house mouse)
C; Superfamily: Multiple (specimal formally form
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JExp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B caracterence number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH0998

A:Accession: 
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Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
Tression: PH0998
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A;Molecule type: mRNA
A;Residues: 1-107 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>
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Search completed: February 14, 2003, 11:19:44

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 14, 2003, 11:05:27; Search time 8.77419 Seconds (without alignments) 80.360 Million cell updates/sec Run on:

US-09-701-001B-2 94 1 EIYPGSGSAYYNEMFKG 17

BLOSUM62 Gapop 10.0 , Gapext 0.5 Perfect score: Sequence: Scoring table:

112892 segs, 41476328 residues rched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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HV02_MOUSE
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                                                                                                                                                                                           "The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";
Eur. J. Immunol. 12:1033-1032(1982).
-!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zakut R., Cohen J., Givol D.;
Nucletc Acids Res. 8:4839-4840(1980).
-!- MISCELLANEDOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
FROM A WYELOWA THAT SECRETES IGG2B.
PIR; A02027; GVWS11.
HSSP; P01810; ZFBJ.
InterPro; IPR003006; Ig_MRC.
InterPro; IPR003506; Ig_V.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                   Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).

Was arguera (Mouse).

Was arguera (Mouse).

Wammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBL_TaxID=10090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-81053741; PubMed-6253904;
Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the cDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
                                                                                                                                                                                                                                                                                                                                                                                                         Score 52; DB 1; Length 120;
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;
                                                                                                                                                         MEDLINE-83131846; Pubmed=6186498;
Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
Marshak-Rothstein A.;
                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region 36-65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                PRT;
                                                                                                                                                                                                                                                               PIR; A02028; HYMSG7.
HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region MPC 11.
                                                                                                                                                                                                                                                                                                                                                                                                     55.3%; 62.5%;
               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 IYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 INPGNGYTKYNEKFKG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1.
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   120
                                     21-JUL-1986
21-JUL-1986
              HV03_MOUSE
P01747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HV01_MOUSE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfan; PF00047; ig; 1. SMART: SW00406; IGv; 1. Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
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                                                                                                                         55.3%; Score 52; DB 1; Length 121; 52.9%; Pred. No. 0.12; Live 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain."; Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51; DB 1; Length 140; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG HEAVY CHAIN V REGION 93G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                NON_TEŘ 121 121
SEQUENCE 121 AA; 13135 MW; 227AEF3EC56EDOBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
gheavy chain V region 93G7 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=82152818; PubMed=6801765;
                                                                                                          Query Match
Best Local Similarity 52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J00493; AAA38128.1; -.
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HSSP; P01810; 2FbJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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50 DIYPGGGFTNYNDNLKG 66
                                                                                                                                                                                                                    1 EIYPGSGSAYYNEMFKG 17
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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21-JUL-1986 (
15-JUL-1999 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Capra J.D.;
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P01748;
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SEQUENCE
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; I.
SMART; SMO0406; IGv; I.
Immunoglobulin V region; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Last annotat
Ig heavy chain V region MOPC 104E.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                            100 EIYKGKANASISIKEYYNDLFK 121
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                                                                                                                                                                                                                                                                                                                   42164 MW;
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                                                                                                                                                                                                                                                                                                                                                45.58;
                                                                                                                                             EMBL; Z36940; CAA85399.1;
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Matches 10; Conservative
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HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                 372 AA;
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                                                (Potential).
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P01756;
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HV12_MOUSE
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                                                                                    Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
 Ig heavy chain V region 23 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Expression and characterization of Campylobacter jejuni
benzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                           COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                             COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                      51.1%; Score 48; DB 1; Length 117; 60.0%; Pred. No. 0.54; ive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                         IG HEAVY CHAIN V REGION 23.
                                                                                                                                                                                                                                                                                                                     12772 MW; C530F829C906F69B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-UNV-2002 (Rel. 41, Last annotation update)
Hypothetical lipoprotein Cj0983 precursor.
                                                                                                                                                                                                                                                                                                  BY SIMILARITY
                                                                                                                                                                                                                                                                       FRAMEWORK-2
                                                                                                                                                                                                                                                                                           FRAMEWORK-3
                                                                                                                                                                                                                                                    FRAMEWORK-1
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    Bacteriol. 177:2396-2402(1995).

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STRAIN=ATCC 43431 / TGH 9011;
MEDLINE=95247673; PubMed=7730270;
                                                                       STRAIN=C57BL/6;
MEDLINE=81234548; PubMed=6788376;
                                                                                                                                                                                                                     Immunoglobulin V region; Signal.
                                                                                                                                                                    HSSP, P01810; 2FBJ.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_V.
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                   449
54
68
85
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                                                                                                                                                             PIR; A02030; HVMS23.
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20
20
50
55
69
86
86
117
117 AA;
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                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                             SEQUENCE FROM N.A.
                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=197;
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P45492; Q9E
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DISULFID
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SEQUENCE
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Biochemistry 21:5415-5424(1982).
-!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Whitehead S., Barrell B.G.; "The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences."; Nature 403:665-668(2000).
                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete amino acid sequence of a mouse mu chain: homology among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3C562051EBC638B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Membrane; Lipoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IN REF. 1)
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MEDLINE-83075344; PubMed-6816276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T -> A (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN HAS ALSO BEEN DETERMINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REF.
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MAY ACTIVATE ATOC BY PHOSPHORYLATION.
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                                                                InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam: PF00047; ig; 1.
SMARY; SM00406; IGv. 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                               1 EIYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                     50 DINPNNGGTSYNOKFKG 66
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                        HSSP; P01789; 1MCP
                                                                                                                                                                                                                             Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia
                                                                                                                                                                                                                                                                                                                                               ATOS_ECOLI
Q06067;
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SEQUENCE
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DOMAIN
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A schilling J., Clevinger B., Davie J. M., Hood L.;

"Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements in heavy chain V-region gene segments.";

Nature 283:55-40(1980).

-! MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO WHICH OCCUR IN THE D AND J SEGMENTS.

-! MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.

PIR: A26242, MHMSJ5.

R SSP; P01789; MMC.

R HSSP; P01789; MC.

R InterPro: IPR0030306; Ig_MHC.

R InterPro: IPR003056; Ig_MHC.

R InterPro: IPR003596; Ig_W.

R Pfam; PF00047; ig; I.

R MART: SMO0406; IGV; I.

T DISULFID

22 96 BY SIMILARITY.
                                                                                         Gaps
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                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-84182519; PubMed-6201362;
Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
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             N-LINKED (GLCNAC. . .) (COMPLEX).
                                                             Score 47; DB 1; Length 117; Pred. No. 0.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%; Score 47; DB 1; Length 117; 47.1%; Pred. No. 0.78;
                                                                                       6; Indels
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22 96 BY SIMILARITY.
55 55 N-LINKED (GLCNAC. . .) (CC
117 117
117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER 117 117 SEQUENCE 117 AA: 13024 MW; 292E2AF4BE447E41 CRC64;
                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
pheavy chain V region J558.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN'1988 (Rel. 06, Created)
01-JAN'1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region AC38 205.12.
Mus musculus (Mouse).
                                                                                     3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
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                                                             50.08;
47.18;
                                                                                                           1 EIYPGSGSAYYNEMFKG 17
                                                                                   8; Conservative
                                                                                                                                  50 DINPNNGGTSYNOKFKG 66
                                                                                                                                                                                              STANDARD;
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les 8; Conservative
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                                                                         Sest Local Similarity
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                                                                                                                                                                                            HV13_MOUSE
P01757;
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P06330;
DISULFID
CARBOHYD
                         NON_TER
SEQUENCE
                                                            Query Match
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HV13_MOUSE
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STRAIN=KI2;

MEDLINE=97251358; PubMed=9097040;

Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
Isono K., Rasai H., Kimura S., Kitakawa M., Kitagawa M.,

Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,

Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,

Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H.,

Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.,

"A 460-Kb DNA sequence of the Escherichia coli K-12 genome

corresponding to the 40.1-50.0 min region on the linkage map.";

DNA Res. 3:379-392(1996).

"FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM ATOS/ATOC;
"A V region determinant (idiotope) expressed at high frequency in B lymphocytes is encoded by a large set of antibody structural genes."; EMBO J. 3:517-523(1984).
PIR; A02040; MHMS38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93348226; Pubmed-8346225; Canifornia B.S., Paterakis A.A., Huang S.-C., Panagiotidis C.A., Kyriakidis D.A.; Indentification, cloning, and nucleotide sequencing of the ornithine decarboxylase antizyme gene of Escherichia coli."; Proc. Natl. Acad. Sci. U.S.A. 90:7129-7133(1993).
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STRAIN=KIZ. / MG1655,
STRAIN=KIZ. / MG1655,
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
May B., Shao Y.,
May B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%; Score 47; DB 1; Length 118; 47.1%; Pred. No. 0.79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                               99 104 D.SCOMENT.
105 118 J.SCGMENT.
22 96 BY SIMILARITY.
118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATOS OR B2219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
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                                                                                                                                                                                                           DISULFID
NON_TER
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                                                                                                                                                                                                                                                                                                                                                    HV05_MOUSE
                                                                                                                              CHAIN
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                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
  -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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PROSITE: PS50113; PAC; 1.
PROSITE: PS50112; PAS; 1.
Sensory transduction; Transferase; Kinase; Phosphorylation; Transmembrane; Inner membrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 1; Length 608; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4669888F98985C9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-0CT-1986 (Rel. 02, Created)
23-0CT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               HISTIDINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V region TEPC 1017 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 138 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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                                                                                                                                                                              InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR004358; Bact_sens_pr_C.
InterPro; IPR004356; HS_KIN_Sig.
InterPro; IPR004356; HIS_KIN_Sig.
InterPro; IPR000561; His_kinA.
InterPro; IPR000700; PAS_assoc_C.
InterPro; IPR000014; PAS_domain.
                                                                                                                                                                                                                                                                                             PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00304; HAMP; 1.
SMART; SM00387; HATPASe_c; 1.
SMART; SM00388; Hisks; 1.
TIGRFAMS; TIGR00229; sensory_box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=84248078; PubMed=6429663;
                                                                                                                                         EMBL; L13078; AAA23449.1; -.
EMBL; AE000311; AAC75279.1; -.
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58.3%;
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                                                                                                                                                                                                                                                    Pfam; PF00512; signal; 1.
Pfam; PF00672; HAMP; 1.
Pfam; PF00989; PAS; 1.
Pfam; PF02518; HATPase_c; 1.
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 FPGIGAGYYNKM 107
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395
6398
398
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608 AA;
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ID HV48_MOUSE
AC P03980;
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TRANSMEM
SEQUENCE
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-!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
                                    Tucker P.W., "Illegitimate recombination generates a class switch from C mu to C ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomı;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V REGION TEPC 1017.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15576 MW; 748157E4C6907B8E CRC64;
                                                                                          delta in an IgD-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
PIR; A02033; HVMST7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAMEWORK-4.
BY SIMILARITY.
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                                                                                                                                                                        HSSP, P01810; ZFBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J00536; AAA38605.1; -. PIR; A02031; HVMS3.
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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Best Local Similarity
9; Conserve
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138
138 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gould S.J., Kalish J.E., Morrel J.C., Bjorkman J., Urguhart A.J.,
Crane D.I.;
                                                                                                                                                                                                                                                             PEX5_PICPA STANDARD; PRT; 576 AA.
13.322; 001967;
01-FEB-1994 (Rel. 28, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Peroxisomal targeting signal receptor (Peroxisomal protein PAS8)
(Peroxin-5), (PTS1 receptor).
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                 0;
                                                 COMPLEMENTARITY - DETERMINING - 1.
                                                                      COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                        Score 45; DB 1; Length 117; Pred. No. 1.7;
                                                                                                                                                                6; Indels
                            IG HEAVY CHAIN V REGION 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                  13016 MW; 427C861C53975EDC CRC64;
                                                                                               BY SIMILARITY.
                                                                                                                                                              2; Mismatches
                                                              FRAMEWORK-2
                                        FRAMEWORK-1
                                                                                   FRAMEWORK - 3
Immunoglobulin V region; Signal.
SIGNAL 1
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46.78;
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                                                                                                                                                                                               Pichia pastoris (Yeast).
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FACTOR (PEX13). SIMILARITY: CONTAINS 7 TPR REPEATS. SIMILARITY: STRONG, TO OTHER PEROXISOMAL TARGETING SIGNAL

RECEPTORS.

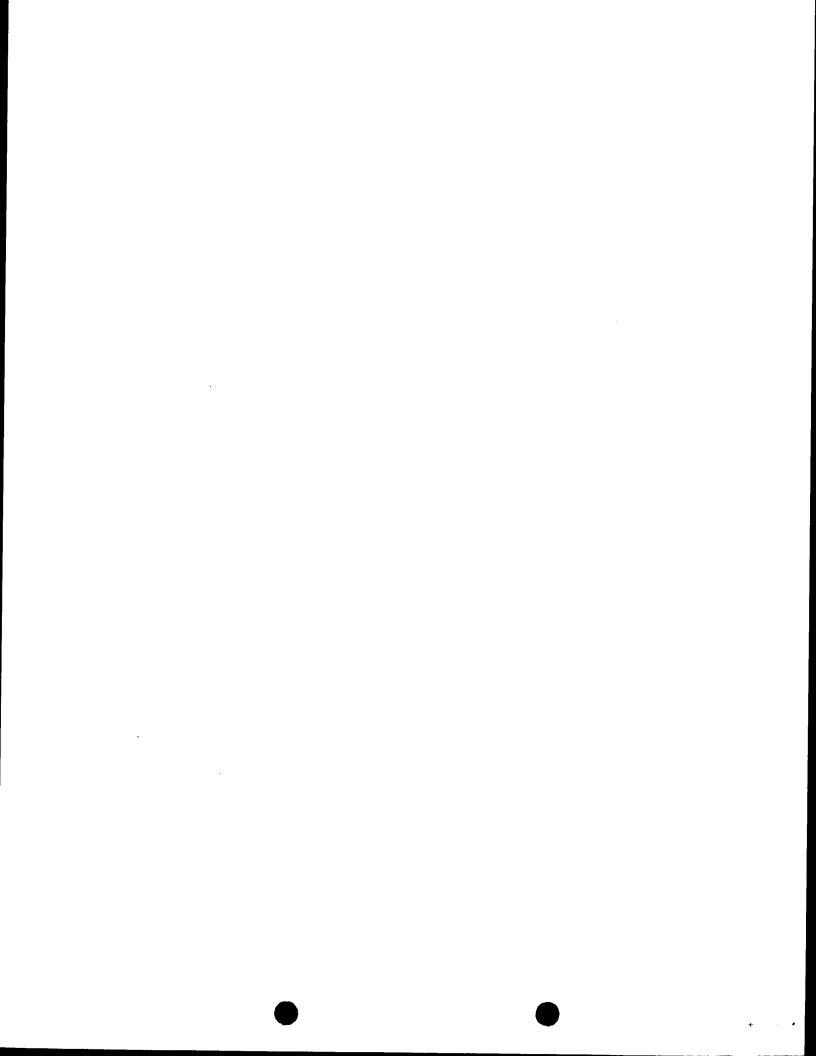
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                               DQFQAQWEKDFAQYAEG -> RPVSGSMGERFCPIRRR
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-!- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION AND IN SYNCYTIUM FORMATION.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human coronavirus (strain OC43).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
E2 91/Yooprotein precursor (Spike 91/Yooprotein) (Peplomer protein)
[Contains: Spike protein S1 (908); Spike protein S2 (90A)].
                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                 TPR repeat; Transport; Protein transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-93389458; PubMed-8376972;
Mounir S., Talbot P.J.;
"Molecular characterization of the S protein gene of human
                                                                                                                                                                                                                                                                                                                      Score 45; DB 1; Length 576; Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                    4; Indels
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C249FBE50FDE5247 CRC64;
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InterPro; IPR002552; Corona_S2.
Pfam; PF01601; Corona_S2; 1.
Glycoprotein; Envelope protein; Transmembrane; Signal.
SIGNAL 1 7 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                   Pred. No. 9.5;
4; Mismatches
                  or send an email to license@isb-sib.ch).
                                                                                                                                                  GLN-RICH.
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TPR 4.
TPR 5.
                                        EMBL; 219592; CAA79640.1; -. EMBL; U59222; AAB40613.1; -. PIR; A40688; A40688. InterPro; IPRO01440; TPR. Pfam; PF00515; TPR; 4. SMART; SM00028; TPR; 4.
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46.78;
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PIR; JQ2168; JQ2168.
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Best Local Similarity
77 Conserve
                                                                                                                               Peroxisome; Repeat;
                                                                                                                                                                                                                                                                                         576 AA;
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Moireau P., Cruciere C., Laporte J.;
"Nucleotide sequence of the glycoprotein S gene of bovine enteric
coronavirus and comparison with the S proteins of two mouse hepatitis
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virus strains.";
J. Gen. Virol. 71:487-492(1990).

- Gen. Virol. 71: PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS
- PUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS
TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovine coronavirus (strain F15).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1901 (Rel. 40, Last annotation update)
E2 glycoprotein precursor (Spike glycoprotein) (Peplomer protein)
[Contains: Spike protein SI (90B); Spike protein S2 (90A)].
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Pred. No. 24;
0; Mismatches 6; Indels
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PIR; A34151; VGIHR1.
InterPro; IPR002552; Corona_S2.
Pfam; PF01601; Corona_S2; 1.
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Transmembrane; Signal
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                   E2 GLYCOPROTEIN.
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SPIKE PROTEIN S2
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Pred. No. 24;
0; Mismatches
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  protein;
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Matches 9; Conserv
  Glycoprotein;
SIGNAL
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GenCore version 5.1.3
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- protein search, using sw model OM protein February 14, 2003, 11:10:17; Search time 35.371 Seconds (without alignments) 99.030 Million cell updates/sec Run on:

1 EIYPGSGSAYYNEMFKG 17 US-09-701-001B-2 94 Title: Perfect score: Sedneuce:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues :paq: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_21:* Database :

sp_vertebrate:*
sp_unclassified:* sp_invertebrate:*
sp_mammal:*
sp_mhc:* sp_rvirus:* sp_bacteriap:* sp_archeap:* sp_organelle:* 1: sp_archea:* 2: sp_bacteria:* sp_plant:* sp_rodent:* sp_virus:* sb_phage:* sp_fungi:* sp_human:* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

+		æ :				
NO.	Score	Match	Match Length DB	DB	ID	Description
	76	80.9		11	Q99LC4	Q991c4 mus musculu
7	7.0	74.5		11	Q9D8L4	Q9d814 mus musculu
m	99	72.3		11	Q9JL83	Q9j183 mus musculu
4	67	71.3		11	Q8VCX7	Q8vcx7 mus musculu
Ŋ	99	70.2		11	092400	Q924q0 mus musculu
9	63	67.0		11	Q91WT1	
7	62	66.0		11	092583	mus
80	62	66.0		11	Q8VDC9	Q8vdc9 mus musculu
σ	59	62.8		11	Q9JL77	Q9j177 mus musculu
10	58	61.7		11	Q99L25	Q99125 mus musculu
11	55	58.5		11	Q9D9B8	Q9d9b8 mus musculu
12	20	53.2		11	Q9Z1C4	Q921c4 mus musculu
13	50	53.2		16	C9WXS7	Q9wxs7 thermotoga
14	48	51.1	121	16	Q8YL22	Q8y122 anabaena sp
15	48	51.1		7	Q9F6B4	Q9f6b4 campylobact
16	48	51.1		11	Q8VCX4	Q8vcx4 mus musculu

1 EIYPGSGSAYYNEMFKG 17

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E G G G L L S S C C C C C C C C C C C C C C C C	Q066291 numan coron Q9qar5 bovine coro Q9qaq8 bovine coro Q91a26 bovine coro Q8v436 bovine coro Q924r5 mus musculu Q924r5 mus musculu Q924r4 mus musculu Q924q4 mus musculu
Q9QXF0 Q9QXE9 Q9TCB6 Q9AZR7 Q9CR10 Q8R3H6 Q921K1 Q80182 Q921K1 Q90R83 Q9DR83 Q9DR82 Q99F82 Q99F82 Q99F80 Q9	0.66291 0.90AR5 0.90A08 0.91A26 0.924 86 0.924 R5 0.924 R5
111 111 112 112 112 112 113 113 113 113	111111111111111111111111111111111111111
1117 1117 1187 1187 1187 1187 1187 1187	1363 1363 1363 1363 1363 137 140
0.000004444444444444444444444444444444	47.9 47.9 47.9 46.8 46.8 46.8
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ Დ
118 119 119 119 110 110 110 110 110 110 110	7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

R MSD; MGI:96446; Igh-4.

R InterPro; IPR003599; Ig-.

R InterPro; IPR003599; Ig-.

R InterPro; IPR003599; Ig-.

R InterPro; IPR003506; Ig-like.

R InterPro; IPR003506; Ig-MHC.

R InterPro; IPR003506; Ig-.

R SMART; SM00409; IG-.

R SMART; SM00409; IG-.

R SMART; SM00409; IG-.

R SMART; SM00410; IG-.

R 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

80.9%; Score 76; DB 11; Length 463;
Best Local Similarity 76.5%; Pred. No. 0.00047;
Matches 13; Conservative 2; Mismatches 2; Indels
                                099LC4;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN cDNA 1810060009 gene.
463 AA
    PRT;
        PRELIMINARY;
                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
    Q99LC4
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Fri Feb 14 15:00:52 2003

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RESULT 5
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X MEDLINE=21085660; PubMed=11217851;

X Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Alazawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Asaito T., Okazaki Y., Gojbori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ratull P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ratull L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Raturich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch R.,

Rayashisaki Y., Roshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havashisaki Y.
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                                                                                                                                                                                      Mus musculus (Mouse),
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.;

"Functional annotation of a full-length mouse cDNA collection.";

"Ature 409:665-690(2001).

EMBL; AK007918; BAB25349.1; -.

HSSP; P01842; 7FAB.

MGD; MI:96443; Igh-1.

InterPro; IPR003599; Ig.

InterPro; IPR003509; Ig_like.

InterPro; IPR003600; Ig_like.

InterPro; IPR003066; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INCELT, T.C., T.C., T.C., SMART; SM00409; IG; 2.
SMART; SM00409; IGc1; 3.
SMART; SM00400; IGc1; 3.
SMART; SM00410; IGc1; 1.
SMART; SM00410; IC_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09JL83;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Last sequence update) U-DEC-2001 (TrEMBLrel. 19, Last annotation update) 1810060009Rik protein. 1GH-1 OR 1810060009RIK.
                                                                               473 AA
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                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                               PRT;
69 EIYPGSGNTYYSEKFKG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EIYPGSGSAYYNEMFKG 17
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                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                            09D8L4;
                                                                          Q9D8L4
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                                             RESULT 2
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Q9JL83
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0
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Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.3%; Score 68; DB 11; Length 110; 75.0%; Pred. No. 0.0019; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Strausberger R.;
Lubmitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC018315; AAR18315.1; -.
R InterPro; IPR003599; Ig.-
R InterPro; IPR003599; Ig.-
R InterPro; IPR003596; Ig.-
R InterPro; IPR003566; Ig.-
R Ffam; PF00047; Ig; 5.
SMART; SMO0409; IG: 2.
R SMART; SMO0409; IG: 1.
R PROSITE; PS00299; IG.-MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.3%; Score 67; DB 11; Length 613; 76.5%; Pred. No. 0.019; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   613 AA; 67855 MW; 41A9384DD4C22862 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 67.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 613 AA.
                                                                                                                                                                                                                                                             streptococca, post...,
with cardiac myosin.";
Infect. Immun. 68:5803-5808(2000).
EMBL; AR206023; ARF69321.1; -.
HSSP; P01810; 2FBJ.
: InterPro; IPR003006; Ig_MHC.
? InterPro; IPR003596; Ig_V.
R Pfam; PR0047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 75.0
Matches 12; Conservative
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TISSUE=SALIVARY GLAND;
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                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                     STRAIN=BALB/C
(Fragment)
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2 IYPGSGSAYYNEMFKG 17
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                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chernajovsky Y.;
                                                                                                                  PubMed=11819679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168
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                                                                                                                                          Su C.;
                                 MRP3
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
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                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                  Kozono Y., Kozono H., Azuma T.;
Pibriect Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).",
Submitted (ANG-2001) to the EMBL/Genbank/DDBJ databases.
EMBL; AB069915; BAB6391.1; -
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                Query Match 70.2%; Score 66; DB 11; Length 143; Best Local Similarity 75.0%; Pred. No. 0.0054; Matches 12; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tisource...;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013499; AAH13490.1;
Interpro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;
                                                                                                                                                                                                                                                                               143 AA; 15704 MW; C99D2433F2BAD8A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     091WT1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 52.1 kDa protein.
                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                          481 AA.
             PRT;
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                                                                  V165-D-J-C mu protein (Fragment).
V165-D-J-C MU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 IYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                                                                                              50 DIYPGSGSTNYNEKFK 65
                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                1 EIYPGSGSAYYNEMFK 16
               PRELIMINARY;
                                                                                                                                                                                                                                                                    143
                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1.
NON_TER 1 1
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                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                     143
                                                                                                                                                         STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=COLON;
                                                                                                                                                                                                                                                                                SEQUENCE
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Cui D., Zeng G., Yan X., Li X., Su C.; "Cloing of intestinal epithelium "Cloing of mouse genes related to repairing of intestinal RNA of mice of the irradiated mice by treatment with the intestinal RNA of mice of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mechanism of exogenous nucleic acids and their precursors improving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the same strain.";
Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
EMBL: AF240166; AAK43731.1; -
InterPro; IPP003006; Ig_MHC.
Pfam: PF00047; ig; 1.
SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the repair of intestinal epithelium after irradiation in mice.", world J. Gastroenterol. 6:709-717(2000).
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EMBL; AJ416332; CAC94867.1; -.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Anti-WOG 212 variable gamma 2a (Fragment).
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 AA.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR001230; Prenyl_site.
Pfam; PF0047; Ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
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111 AA.
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68.8%;
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 68.8
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 IYPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 IYPRDGSTKYNEKFKG 85
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                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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0
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0
                                                                  66.0%; Score 62; DB 11; Length 168; 70.6%; Pred. No. 0.029; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.8%; Score 59; DB 11; Length 110; 64.7%; Pred. No. 0.055; Live 1; Mismatches 5; Indels
                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC003888; AAH03888.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
SEQUENCE 168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 110
110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with cardiac myosin.";
Infect. Immun. 68:5803·5808(2000).
EMBL: AF2060029; AAF69327.1;
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20448942; PubMed=10992488;
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InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART. SMO0406; IGV; 1.
NON_TER 1 1 1
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InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                              69 EILPGSGRINYNEKFKG 85
                                                                                                                                                                                            1 EIYPGSGSAYYNEMFKG 17
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EIYPGSGSAYYNEMFKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 64.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                           Query Match
Best Local Similarity
Matches 12; Conserv
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NON_TER
SEQUENCE
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RA STARIN—CSTBL/6J; TISSUE=TESTIS;

RA KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Alawai J., Shinagawa H., Kinbata K., Kondo H., Kadachi J., Fukuda S.,

Alawai Y., Izawa M., Nishi K., Kino B., Kanamaka I.,

RA Salto T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

R. Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Mikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Wikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Blowstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Cariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchioni L., Mashima J., Mazaraelli J., Mombaerts P.,

RA Scarki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Wynshaw-Bolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).

Muscarlus (Mouse).

Muscarlus Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
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"Functional annotation of a full-length mouse cDNA collection.";
Wature 409:685-690(2001).
EMBL; AK007163; BAB24877.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 58; DB 11; Length 473;
Pred. No. 0.41;
0; Mismatches 5; Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Adult male testis cDNA, RIKEN full-length enriched library,
clone:1700110111, full insert sequence.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam, PF00047; Ig; 3.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv. 1.
SMART; SM00410; IGl.; 3.
SMART; SM00410; IGl.ke; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SRART; AND A, 52449 MW; BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSF; FULLLY, ELC., HSF; FULLY, ELC., HSF; FULLY, ELC., IPR003599; Iq. InterPro; IPR003600; Iq.like. InterPro; IPR003560; Iq.MHC. InterPro; IPR003566; Iq.V. Pfam; PF00047; Iq. I. SMART; SM00409; IG; I. SMART; SM00406; IGV; I. SMART; SM00410; IG_like; I. SEQUENCE 111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64;
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RESULT 14
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DDT
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OOC
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MEDLINE=99287316; PubMed=10360571;
MEDLINE=99287316; PubMed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                    STRAIN=BALB/C;
Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
Matis L.M., Evans M.J.;
"Humanized porcine VCAM-specific monoclonal antibodies with chimeric
IgG2/64 constant regions block human leukocyte binding to porcine
endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50; DB 11; Length 118;
Pred. No. 1.7;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U78801; AAD00293.1; -.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
011gopeptide ABC transporter, permease protein.
TM0072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 AA.
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                                                                                          PRT;
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Pfam; PF00528; BPD_transp; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.2%;
50.0%;
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InterPro; IPR003596; Ig_V.
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Matches 8; Conservative
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    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                    Gaps
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Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
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                                                         Length 335;
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                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA RES. 8:205-213(2001).

EMBL; AP003600; BAB78200.1; -.

Plasmid; Hypothetical protein; Complete proteome.

SEQUENCE 121 AA; 13184 MW; 79E76CFB575E96E3 CRC64;
              38222 MW; 653D1AA484DC9FF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein All7116.
                                                       53.2%; Score 50; DB 16; 60.0%; Pred. No. 5.5;
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                                                                                                                                                                                                                                                                                                                 121 AA
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                                                                                                       1; Mismatches
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MEDLINE=21595285; PubMed=11759840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anabaena sp. (strain PCC 7120).
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                                                                                                            Conservative
                                                                                                                                                                                 1|| || || || 284 YPGIGSLLYNAIFTG 298
                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                    3 YPGSGSAYYNEMFKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pcc7120alpha.
Complete proteome. SEQUENCE 335 AA;
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Best Local Similarity
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                                                                               Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=103690;
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Ouery Match
Best Local Similarity 45.5%; Pred. No. 13;
Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 1;
Oy 1 EIYPGSGSA-----YNEMFK 16
Db 100 EIYRGEANASISIKEYYNDEFK 121
Search completed: February 14, 2003, 11:18:37
Job time: 36.5376 secs
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February 14, 2003, 11:04:17; Search time 24.3871 Seconds (without alignments) 49.176 Million cell updates/sec
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                        908470 seqs, 133250620 residues
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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50
1 RGTGTGFAY 9
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Perfect score:
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Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:* 2: SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:* 3: SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:* 4: SIDS2/gcgdata/geneseqf-embl/AA1982.DAT:* 5: SIDS2/gcgdata/geneseqf-embl/AA1983.DAT:* 6: SIDS2/gcgdata/geneseqf-embl/AA1986.DAT:* 7: SIDS2/gcgdata/geneseqf-embl/AA1986.DAT:* 8: SIDS2/gcgdata/geneseqf-embl/AA1986.DAT:* 9: SIDS2/gcgdata/geneseqf-embl/AA1980.DAT:* 10: SIDS2/gcgdata/geneseqf-embl/AA1980.DAT:* 11: SIDS2/gcgdata/geneseqf-embl/AA1980.DAT:* 12: SIDS2/gcgdata/geneseqf-embl/AA1991.DAT:* 13: SIDS2/gcgdata/geneseqf-embl/AA1991.DAT:* 14: SIDS2/gcgdata/geneseqf-embl/AA1991.DAT:* 15: SIDS2/gcgdata/geneseqf-embl/AA1991.DAT:* 16: SIDS2/gcgdata/geneseqf-embl/AA1991.DAT:* 17: SIDS2/gcgdata/geneseqf-embl/AA1991.DAT:* 18: SIDS2/gcgdata/geneseqf-embl/AA1995.DAT:* 18: SIDS2/gcgdata/geneseqf-embl/AA1995.DAT:* 18: SIDS2/gcgdata/geneseqf-embl/AA1995.DAT:* 19: SIDS2/gcgdata/geneseqf-embl/AA1995.DAT:* 10: SIDS2/gcgdata/geneseqf-embl/AA1995.DAT:* 10: SIDS2/gcgdata/geneseqf-embl/AA1995.DAT:* 11: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:* 12: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:* 13: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:* 14: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:* 15: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:* 16: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:* 17: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:* 18: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:* 19: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:* 20: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:* 21: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:* 21: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:* 22: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:* 23: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:* 24: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:* 25: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:* 27: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:* 27: SIDS2/gcgdata/geneseqf-embl/AA1999.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					COTTON TO CO	
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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	1 1 1 1 1 1		1 1 1 1 1 1	1		
_	50	100.0	σ	21	AAY59258	Antibody 4H5 H cha
10	50	100.0	6	21	AAY51135	Murine CD4/CD34 re
· "	50	100.0		21	AAY59262	Antibody 4H5 H cha
4	50	100.0		21	AAY51139	Murine derived pro
· to	20	100.0		21	AAY59266	Antibody 4H5 H cha
·	50	100.0		21	AAY51143	Murine derived pro
7	50	100.0		21	AAY51145	Murine derived pro
· 00	050	100.0		21	AAY59264	Antibody 4H5 H cha
σ	50	100.0		21	AAY59265	Antibody 4H5 L cha
10	50	100.0	305	21	AAY51141	Murine derived pro

The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and

Claim 1; Page 14; 25pp; Japanese.

Murine derived pro Hepatitis B virus Hepatitis B virus Hepatitis B virus Anti-Leu 3a heavy Anti-Leu 3a heavy Anti-Leu 3a peavy Human G protein-co Murine clodin prot Murine clodin 3 pr Zebrafish atonal h Amino acid sequenc Human prostate can Propionibacterium Propionibacterium Propionibacterium Corynebacterium gil C glutamicum prote Human pancreatic c N.meningtidis 239 Sequence of low mo Bovine rotavirus S Human differentiat	Human immune/haema Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Fragment of human Fragme
AAY51142 AAU70016 AANU70768 AAR04135 AAR04133 AAR04133 AAR04133 AAX151679 AAY51679 AAY51679 AAY51679 AAY48329 AAY48329 AAN96343 AAN96343 AAN96343 AAR96366 AAR96343 AAR96343 AAR96368 AAR34401 AAR34401 AAR34401 AAR34401 AAR34401 AAR34401 AAR34401 AAR34401 AAR34401	
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305 120 122 1122 1122 1136 1145 1145 1145 1145 1145 1145 1145 114	251 105 105 105 134 134 134 135 137 137 137 137 137 137 137 137 137 137
1000.0 888.0 888.0 880.0 174.0 174.0 170.0 170.0 170.0 170.0 170.0 170.0 170.0 170.0 170.0 170.0 170.0 170.0 170.0 170.0 170.0	
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11 12 12 14 15 16 16 16 17 18 17 18 17 18 18 19 20 20 20 20 20 20 20 20 20 20 20 20 20	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

An antibody and the nucleic acid coding the antibody Antibody 4H5 H chain variable region CDR3 fragment. CD4 antigen; anti-human; antibody; 4H5; drug; CDR; complementarity determining region. AAY59258 standard; peptide; 9 AA. (ASAH) ASAHI KASEI KOGYO KK. 98JP-0163034. 98JP-0163034. 17-APR-2000 (first entry) WPI; 2000-091351/08. JP11332563-A. 26-MAY-1998; 26-MAY-1998; 07-DEC-1999. AAY59258; Mus sp. RESULT 1 AAY59258

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived complementarity determining the compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived complementarity determining the complementarity determinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells
application for drugs. It is highly safe in human dose. Sequences AAX59256-58 represent the complementarity determining region (CDR)-1, CDR-2 and CDR-3 fragments in the H chain variable region of the
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine CD4/CD34 recognizing antibody heavy chain CDR-3 region #1.
                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                               100.0%; Score 50; DB 21; Length 9; 100.0%; Pred. No. 7.8e+05; Live 0; Mismatches 0; Indels
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100.0%; Pred. No. 7.8e+05;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY51135 standard; Protein; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 76; 111pp; Japanese.
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(ASAH ) ASAHI MEDICAL CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDR-3; heavy chain; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98JP-0163023
                                                                                        antibody 4H5 respectively.
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                                                                                                                                                                                                                                                          Conservative
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the H chain variable region of the antibody 4H5.
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                                                                                                                          CD4 antigen; anti-human; antibody; 4H5; drug.
                                                                                           Antibody 4H5 H chain variable region.
AAY59262 standard; protein; 110 AA.
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                                                                                                                                                                                                                                                                                                              (ASAH ) ASAHI KASEI KOGYO KK
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Query Match
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                                                                                                                                                                                                                                                This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents a H chain fragment of the antibody 4H5.
                                                                                                                                                                        Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells \,
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                                                                                                Soka T, Morimoto I, Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 22; 25pp; Japanese.
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                                                                                                                                                                                                                            Claim 22; Page 78; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody 4H5 H chain fragment
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     98JP-0159957.
98JP-0163023.
                                                   (ASAH ) ASAHI KASEI KOGYO KK
                                                                 (ASAH ) ASAHI MEDICAL CO LTD
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Best Local Similarity luv...
Lea 9; Conservative
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     25-MAY-1998;
26-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
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                                          21; Length 118;
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100.0%; Pred. No. 0.45;
                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                         AAY51143 standard; Protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine derived protein fragment #5.
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                                                                           Best Local Similarity 100.
Matches 9; Conservative
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118 AA;
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Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
9; Conserve
                                                                                             WPI; 2000-091351/08
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                                                                                                                                                                                                                       305 AA;
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                                                                                                         N-PSDB; AAZ58663
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                                   26-MAY-1998;
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               07-DEC-1999.
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                                                                              Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoletic undifferentiated cells, elimination of Lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD4 antigen; anti-human; antibody; 4H5; drug.
                                                                                                                                                                                                                                                                   Soka T, Morimoto I, Miyamura K;
                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 96-97; 111pp; Japanese.
AAY51145 standard; Protein; 118 AA.
                                                             Murine derived protein fragment #7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody 4H5 H chain sequence.
                                                                                                                                                                                                                                   (ASAH ) ASAHI KASEI KOGYO KK.
(ASAH ) ASAHI MEDICAL CO LTD.
                                                                                                                                                                                                                98JP-0163023.
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                                      31-MAR-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 RGTGTGFAY 107
                                                                                                                                                                                                                                                                                                 N-PSDB; AAZ44231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGTGTGFAY 9
                                                                                                                                           WO9961629-A1.
                                                                                                                                                                                  24-MAY-1999;
                                                                                                                                                                                                      25-MAY-1998;
26-MAY-1998;
                                                                                                                                                               02-DEC-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-APR-2000
                    AAY51145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY59264;
                                                                                                                       Mus sp.
                                                                                                                                                                                                                                                                  Ono M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tches
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                                                                                                                                                                                                                                                                                                                                                                The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the H chain sequence of the antibody 4H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the L chain sequence of the antibody 4H5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 50; DB 21; Length 305; 100.0%; Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                  An antibody and the nucleic acid coding the antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD4 antigen; anti-human; antibody; 4H5; drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                             Disclosure; Page 16-17; 25pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY59265 standard; protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody 4H5 L chain sequence.
                                                                                                              (ASAH ) ASAHI KASEI KOGYO KK
                                                     98JP-0163034.
98JP-0163034.
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01-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
                                                                                                                                                         Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                                             Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells \,^{\circ}
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                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 22; Page 80-82; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY51142 standard; Protein; 305 AA.
                                                                                                                                         Murine derived protein fragment #3.
                                                                               AAY51141 standard; Protein; 305 AA.
                                                                                                                                                                                                                                                              99WO-JP02711.
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                                                                                                                       31-MAR-2000 (first entry)
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Best Local Similarity
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247 RGTGTGFAY 255
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                       1 RGTGTGFAY 9
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           1 RGTGTGFAY 9
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                                                                                                   AAY51141;
                                                                                                                                                                                                       Mus sp.
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AAY51142
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Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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98JP-0159957.
98JP-0163023.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soka T, Morimoto I, Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 22; Page 82-84; 111pp; Japanese.
Murine derived protein fragment #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ASAH ) ASAHI MEDICAL CO LTD.
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Best Local Similarity
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The invention relates to an isolated or purified peptide (I) which binds Hepatitis B virus (HBV) core antigen (HBCAG) or HBV E antigen (HBCAG).

(I) is useful for treating or preventing Hepatitis B virus (HBV).

(I) is useful for treating or preventing Hepatitis B virus (HBV).

(I) is also useful

for determining the presence of HBV in a biological sample, and for inhibiting B cell mediated processing and uptake of HBCAG and/or HBEAG, by determining whether (I) inhibits B cell mediated processing and protessing and assay of T cell

or proliferation or cytokine production. (I) is also useful for modulating an immune system response. (I) is useful as a template for a design of synthetic molecules including peptides, derivatives or modified peptides, coll, diagnostic reagent and as active ingredient in pharmaceuticals.

(I) is also useful as detection reagents in conventional collogical sample, and to determine the efficacy of an HBV treatment placed and to determine the efficacy of an HBV treatment processing the levels of HBCAG and/or HBBAG during and after antigen (HBCAG) or HBV E antigen (HBCAG) binding partners as described in the invention
                                                                                                                                                                                            Novel peptide that binds to hepatitis B virus core or E antigen, useful for treating and preventing hepatitis B virus infection .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory; HBV core antigen; HBcAg; HBV E antigen; HBcAg;
B cell mediated processing; T cell proliferation; cytokine production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis B virus; virucide; immunomodulator; hepatotropic; HBV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis B virus antigen binding partner 9C8 VH.
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88.9%; Pred. No. 0.8;
Live 0; Mismatches
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                                                                                                                                                                                                                                                 Claim 2; Page 33; 82pp; English.
                20-APR-2001; 2001WO-IB00844.
                                                21-APR-2000; 2000US-0556605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-APR-2001; 2001WO-IB00844.
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                                                                                                                                                         WPI; 2002-055347/07.
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Best Local Similarity
Matches 8; Conserv
                                                                                      (TRIP-) TRIPEP AB.
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                                                                                                                       Sallberg M;
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The invention relates to an isolated or purified peptide (1) which binds Hepatitis B virus (HBV) core antigen (HBCAG) or HBV E antigen (HBCAG).

(1) is useful for treating or preventing Hepatitis B virus (HBV).

(2) infection, by identifying a subject in need of a molecule that inhibits infection, and providing the subject with (1). (1) is also useful for determining the presence of HBV in a biological sample, and for inhibiting B cell mediated processing and uptake of HBCAG and/or HBCAG.

(3) by determining whether (1) inhibits B cell mediated processing and uptake of HBCAG and/or HBCAG.

(4) by determining whether (1) inhibits B cell mediated processing and uptake of HBCAG and/or HBCAG.

(5) by determining whether (1) inhibits B cell mediated processing and proliferation or cytokine production.

(6) proliferation or cytokine production.

(7) is also useful as a template for a design of synthetic molecules including peptides, derivatives or modified peptides, peptidomimetics and chemicals.

(1) is also useful as detection reagents in conventional impunchistochemical techniques, as diagnostic reagents to detect HBV in biological sample, and to determine the efficacy of an HBV treatment biological sample, and to determine the efficacy of an HBV treatment processing and in the invention.
                                                                                                                  Novel peptide that binds to hepatitis B virus core or E antigen, useful for treating and preventing hepatitis B virus infection
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88.9%; Pred. No. 4.9;
.ive 0; Mismatches 1; Indels
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                                                                                                                                                                      Claim 2; Page 11; 82pp; English.
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                                                                                     WPI; 2002-055347/07.
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                (TRIP-) TRIPEP AB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 AA;
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                                               Sallberg M;
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                                                                     Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be used to form chimeric mouse-variable, human-constant region Abs suggested as being useful as a vaccine to HIV.
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80.0%; Score 40; DB 11; Length 136;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                       Query Match 80.0%; Score 40; DB 11; Length 122; Best Local Similarity 77.8%; Pred. No. 21; Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New chimeric variants of murine antibody anti-leucine -
contg. human antibody regions, and DNA encoding sequences.
    New chimeric variants of murine antibody anti-leucine -contg. human antibody regions, and DNA encoding sequences.
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                                                 Claim 5; Fig 5; 12pp; English.
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|17 RGKGTGFAF 125
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                                                                                                                                                                                                                                    103 RGKGTGFAF 111
                                                                                                                                    122 AA;
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                                                                                                                                     Sequence
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                                                                                                              Pebruary 14, 2003, 11:13:07 ; Search time 8.12903 Seconds
(without alignments)
32.575 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-156-605-3

US-09-156-605-3

US-08-064-174-1

US-08-064-174-1

US-08-064-174-1

US-08-064-174-1

US-08-313-1

US-08-313-750C-44

US-09-314-613-44

US-08-434-255-8

US-08-449-957-8

US-08-459-871-8

US-08-459-871-8

US-09-010-623A-2

US-09-010-623A-2

US-09-010-623A-2

US-09-011-359A-2

US-09-011-359A-2

US-09-011-359A-2

US-08-459-967-6

US-08-459-967-6

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US-08-459-871-6

US-08-459-871-6

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US-08-459-871-6

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US-08-459-967-2
US-08-459-967-4
US-08-460-327-2
                                                                                                                                                                                                                                                                                                                                   262574 seqs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence 4, Appli Sequence 2, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 61, Appli Sequence 2, Appli Sequence 2, Appli Sequence 68, Appli Sequence 68, Appli Sequence 68, Appli Sequence 68, Appli Sequence 18, Appli Sequence 2, Appli Sequence 3, Appli Sequence 4, Appli Sequence 68, Appli Sequence 68, Appli Sequence 68, Appli Sequence 68, Appli Sequence 68, Appli Sequence 68, Appli		W	20; .ls 0; Gaps		· •
US-08-460-327-4 US-08-459-871-2 US-08-459-871-4 US-08-296-791-2 PCT-US95-10661A-2 US-09-134-001C-4238 US-09-134-01C-4238 US-09-134-01C-4238 US-09-624-183-2 PCT-US95-2 US-09-624-183-2 US-09-624-183-2 US-09-624-183-2 US-09-005-069-68 US-09-171-156A-27 US-09-171-156A-27 US-08-460-309-2 US-08-125-077-2 US-08-125-077-2 US-08-125-077-2	ALIGNMENTS	RESULT 1 Sequence 36, Application US/09556605 Sequence 36, Application US/09556605 Patent No. 6417324 GENERAL INFORMATION: APPLICANT: Balberg, Matti APPLICANT: Lazdina, Una TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS FILE REPERENCE: TRIPEP.020A CURRENT APPLICATION NUMBER: US/09/556,605 CURRENT FILING DATE: 2000-04-21 NUMBER OF SEQ ID NOS: 78 SEQ ID NO 36 LENGTH: 20 SEQ ID NO 36 LENGTH: 20 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: COTHER INFORMATION: Artificial Oligonucleotide COTHER INFORMATION: Artificial oligonucleotide	Score 44; DB 4; Length 20 Pred. No. 0.29;); Mismatches 1; Indels		1556605 C PEPTIDES THAT BIND TO THE IS B VIRUS CORE AND E ANTIGENS US/09/556,605 1-21 vs Version 4.0
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397 397 397 1394 1394 2348 348 348 361 461 659 1130 1130		ion US Matti Matti Una	88. larity 88. Conservative		ion US/0955 Matti SMATHETIC HEPATITIS PEP.020A PUMBER: US : 2000-04-2 S: 78 or Windows
00000000000000000000000000000000000000		LT 1 quence 36, Application US/09556605 quence 36, Application US/09556605 tent No. 641734 NERAL INFORMATION: PPLICANT: Sallberg, Matti PPLICANT: Lazdina, Una ITLE OF INVENTION: SWITHETIC PEPTIDE: ITLE OF INVENTION: SWITHETIC PEPTIDE: ILE REFERENCE: TRIPED: 0.20A URRENT APPLICATION NUMBER: US/09/556 UMBER OF SEQ ID NOS: 78. OFTWARE: PASLSEQ for Windows Version 0. ID NO 36 LENGTH: 20 LENGTH: 20 TYPE: RT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Artificial Oligon 09-556-605-36	h Similarity 8; Conserv	GFAY 9	pplicat 7324 AMIDON: AMIDON: AMIDON: SWTION: SWTION: SWTION: CATION OG DATE
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		SULT 1 Squence 36, A Sequence 36, A Batent No. 641 GENERAL INFORM APPLICANT: La APPLICANT: La TITLE OF INVE TITLE OF INVE FILE REFRENC CURRENT APPLI CURRENT APPLI CURRENT FILIN NUMBER OF SEQ SOFTWARE: FAS SEQ ID NO 36 IENGTH: 20 IENGTH: 20 IENGTH: 20 IENGTH: 20 IENGTH: 20 IENGTH: 20 IENGTH: 30 IENGTH: 30 IENGTH: 30 IENGTH: 30 IENGTH: 30 INFORM ORGANISM: AF FEATURE: FEATURE: OFGANISM: AF FEATUR	y Match Local Si hes 8;	1 RGTGTGFAY 7 RGKGTGFAY	LT 2 9-556-605-3 quence 3, Ag tent No. 641 NERAL INFORM PPLICANT: ES PPLICANT: LE TITLE OF INVI ITLE REPEREN URRENT APPLI URRENT FILLI URRENT FILLI URBER OF SE OF TENT URBER OF SE URBER OF SE OF TENT URBER OF SE URBER
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TYPE: PRT ORGANISM: Artificial Sequence FEATURE:

Sequence 4, Sequence 2,

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FILING DATE: 03-OCT-1991
ATTORNEY/AGENT INFORMATION:
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US-08-066-167-1
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APPLICANT: HOltzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TILE OF INVENTION: TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
ILE REFERENCE: 09404/041001
CURENT APPLICATION NUMBER: US/09/130,491
CURENT FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-08-06
SEALIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 247
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APPLICANT: QUENTIN-MILLET, Marie-Jose
APPLICANT: LISSOLO, LING
TITLE OF INVENTION: SUBBUTT VACCINE FOR NEISSERIA
TITLE OF INVENTION: MENINGITIDIS INFECTIONS AND CORRESPONDING PURIFIED
TITLE OF INVENTION: SUBBURTS
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                                                                                                                           88.0%; Score 44; DB 4; Length 130; 88.9%; Pred. No. 1.8;
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CORRESPONDENCES:

CORRESPONDENCES:

CORRESPONDENCES:

CORRESPONDENCES:

STREET:

CITY:

Alexandria

COUNTRY:

Alided States

ZIP:

Z1P:

Z2313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE:

Floppy disk

COMPUTER:

COMPUTER
                                                                                                                                                                                                                    1; Indels
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; OTHER INFORMATION: Artificial Oligonucleotide US-09-556-605-3
                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/064,174
FILING DATE: 25-MAY-1993
CLASSIFICATION: 424
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; Sequence 1, Application US/08064174
; Patent No. 5618540
                                                                                                                                Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens US-09-130-491-15
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97 RGKGTGFAY 105
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US-09-130-491-15
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APPLICANT: QUENTIN-MILLET, Marie-Jose
TITLE OF INVENTION: VACCINE AGAINST NEISSERIA MENINGITIDIS
TITLE OF INVENTION: WACCINE AGAINST NEISSERIA MENINGITIDIS
TITLE OF INVENTION: WACCINE AGAINST NEISSERIA MENINGITIDIS
TITLE OF INVENTION: WESCINOS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STREET: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER: FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 1; Length 579; Pred. No. 2.1e+02; 1; Mismatches 2; Indels
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US-08-066-167-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 016100-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/836-6620
TELEFAX: 703/836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                016100-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/066,167
FILING DATE: 02-UUN-1993
CLASSIFICATION: 424
PLIASSIFICATION DATA:
APPLICATION NUMBER: FR 91 12177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Crane-Feury, Sharon E
REGISTATION UNBER: 36,113
REFERENCE/DOCKET NUMBER: 01610
TELECOMMUNICATION INFORMATION:
TELEFAN: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08066167 Patent No. 5618541
                                                                                                                                                                                                                                                                                                                                                                    70.08;
66.78;
                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 03-OCT-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 579 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66./v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-064-174-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein ORIGINAL SOURCE:
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DB 1; Length 579;

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; Sequence 10, Application US/09314242A
; Sequence 10, 6248575
; GENERAL INFORMATION:
; THEO FUNCHION: Useleic Acids Encoding Polypeptides
; TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
; TITLE OF INVENTION: Having L-Amino Acid Oxidase Activity
FILE REPERENCE: 5566.200-US
; CURRENT APPLICATION NUMBER: US/09/314,242A
; CURRENT FILING DATE: 1999-05-18
; EARLIER FILING DATE: 1998-05-18
; WUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.0%; Score 34; DB 4; Length 20; 75.0%; Pred. No. 12; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/671,978A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: GOLRICK, MARY E
REFERENCE/DOCKET NUMBER: 22727/00133
TELECOMMULCATION INFORMATION:
TELEPHONE: (216) 622-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 2; Ler
Pred. No. 2.3e+02;
                                                                              SSEE: CALFEE, HALTER & GRISWOLD STAND SUPERIOR AVENUE, SUITE 1400 CLEVELAND
APPLICANT: Kim, Wonyong
APPLICANT: Chang, Keong-OK
TITLE OF INVENTION: ROTAVIRUS GENES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Trichoderma harzianum
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (216) 622-8200
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.0%;
85.7%;
                                                                                                                                                                             ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 640 amino acids
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Best Local Similarity
'Local 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 TGTGFAY 9
                                                                                                                                                OHIO
                                                                                           ADDRESSEE:
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                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 10
LENGTH: 20
                                                                                                              STREET:
                                                                                                                                             STATE:
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APPLICANT: QUENTIN-MILLET, Marie-Jose
APPLICANT: LISSOLO, Ling
TITLE OF INVENTION: SUBUNIT VACCINE FOR NEISSERIA
TITLE OF INVENTION: MENINGITIDIS INFECTIONS AND CORRESPONDING PURIFIED
TITLE OF INVENTION: SUBUNITS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                      Gaps
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                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.0%; Score 35; DB 2; Lei
66.7%; Pred. No. 2.1e+02;
   Pred. No. 2.1e+02;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                        BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FF 91 12176
FILING DATE: 03-OCT-1991
PRIOR APPLICATION NUMBER: 08/064,174
FILING DATE: 25-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Virginia
COUNTRY: United States
LIP. 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-671-978A-10
Sequence 10, Application US/08671978A
Patent No. 5959093
GENERAL INFORMATION:
APPLICANT: Salf, Linda J.
APPLICANT: Parwani, Anil
                                                                                                                                                                                     Sequence 1, Application US/08449733 Patent No. 5928650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 703/836-2021 NFORMATION FOR SEQ ID NO: 1:
     66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          579 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
     Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BURNS, DOAN
STREET: P.O. Box 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   703/836-2021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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Best Local Similarity
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                                                                                             442 RGTGTWYGY 450
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                                                         1 RGTGTGFAY 9
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US-08-449-733-1
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ADDRESSEE: No. 56210890 No. 5621089disk of No. 5621089th America, Inc. STREET: 405 Lexington Avenue, 64th Floor
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                                                                                         TITLE OF INVENTION: HUMAN REGULATORY MOLECULES NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
FILLIG DATE:
                                                                                                                                                         E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PF-0356 US TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sloma, Alan P.
APPLICANT: Sloma, Helle
APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Aaslyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 8, Application US/08434255; Patent No. 5621089; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: THPINOTO3
CLONE: 2469611
US-09-234-613-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.00
Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
  Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA ZIP: 10174-6401 COMPUTER READABLE FORM:
                                                                                                                                                                           STREET: 3174 Por
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
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                                                                                                                                                                                                                                  COUNTRY: US
                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-434-255-8
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STATE:
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Pred. No. 1.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                APPLICANT: 1410.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
CORRESPONDENCE: 98
CORRESPONDENCE: ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOPTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION DATA:
APPLICATION NUMBER: APPLICATION NUMBER:
FILING DATE: ATTORNEY-AGENT INFORMATION:
NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-0356 US
TELEPHONE: 415-85-0555
TELEPHONE: 415-85-0555
                                                                                                                                                                                                                                                                                                                            STREE: SATE: DATE: CA
                                                                       US-08-933-750C-44
; Sequence 44, Application US/08933750C
; Betent No. 5932442
; GENERAL INFORMATION:
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Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 44: SEQUENCE CHARACTERISTICS: LENGTH: 251 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LIBRARY: THP1NOT03
; CLONE: 2469611
US-08-933-750C-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear IMMEDIATE SOURCE:
3 RGTNTGYA 10
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| 65 GPGTGFLY 72
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US-09-234-613-44
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Sequence 8, Application US/08459871 Patent No. 5650326 GENERAL INFORMATION:
                                                                                                                                                                                                                                                         US-08-460-327-8
; Sequence 8, Application US/08460327
; Patent No. 5622850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 280 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sloma, Alan P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.03
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-08-460-327-8
                                                                                                          Conservative
           , MOLECULE TYPE: protein US-08-459-967-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10174-6401
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 GTGTNFKY 269
                                                                                                                                                                                262 GTGTNFKY 269
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                                                                                                                                             2 GTGTGFAY 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 1; Length 280;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                           COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3764.400-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 433

CLASSIFICATION: 433

PRICATION NUMBER: US 08/434,255

PILING DATE: 03-MAY-1995

ATTORNEY/AGENT INFORMATION:
NAME: Agris Dr., Cheryl H.
REGISTRATION NUMBER: 34,086

REFERENCE/DOCKET NUMBER: 3764.400-US

TELECHOME: 212-867-0123

TELEPHOME: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Dasalyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                3764.400-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/459,967
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08459967
Patent No. 5622841
GENERAL INFORMATION:
                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Agris Dr., Cheryl H.
REGISTRATION UNDRER: 34,084
REFERENCE/DOCKET 134,084
REFERENCE/DOCKET 134,084
TELECOMMUNICATION INFORMATION:
TELEPAN: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 280 anino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                        68.0%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 280 amino acids TYPE: amino acid
         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sloma, Alan P.
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.0v
-Loca 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-08-434-255-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                         FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10174-6401
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262 GTGTNFKY 269
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APPLICANT: Sloma, Alan P.
APPLICANT: Sloma, Helle
APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Asslying, Dorrit
ITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56228500 No. 5622850disk of No. 5622850th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
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68.0%; Score 34; DB 1; Length 280; 75.0%; Pred. No. 1.5e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10174-640.

ZIP: 10174-640.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
FILING DATE: 02-UN-1995
FILING DATE: 02-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 3764.400-US TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123 TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR AFFLICATION UNDBER: US 08/434,255
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: AGTIS Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
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ADDRESSEE: No. 56503260 No. 5650326disk of No. 5650326th America, Inc. STREET: 405 Lexington Avenue, 64th Floor CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,871
FILING DATE: 02-7UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/434,255
FILING DATE: 03-MX-1995
ATTORNEY/AGENT INFORMATION:
NAME: APPLICATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764.400-US
REJECTRATION NUMBER: 376.086
REFERENCE/DOCKET NUMBER: 376.086
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Patent No. 624501
GENERAL INFORMATION:
APPLICANT: VON der Osten, Claus
APPLICANT: Olsen, Arne Agerlin
APPLICANT: Rewin Ludo
ITLE OF INVENTION: A modified Polypeptide
FILE REFERENCE: 4923.204-US
CURRENT FILING DATE: 1998-02-17
EARLIER APPLICATION NUMBER: US/09/024,532
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT/DK98/00046
EARLIER FILING DATE: 1997-02-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 280
APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Aaslyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 280 amino acids
amino acid
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Best Local Similarity 75.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-459-871-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: bacillus sp.
US-09-024-532-2
                                                                                                                                                                                                                                                                                                     STATE: New YORK COUNTRY: USA ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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262 GTGTNFKY 269
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9-024-532-2
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Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps
Qy 2 GTGTGFAY 9
Illi | |
Db 262 GTGTNFKY 269
Search completed: February 14, 2003, 11:20:48
Job time: 9.12903 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 14, 2003, 11:15:53; Search time 5.22581 Seconds (without alignments) 44.001 Million cell updates/sec Run on:

US-09-701-001B-3 50

1 RGTGTGFAY 9 Perfect score: Sednence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

140259 seqs, 25548876 residues rched: al number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

Published_Applications_AA:*

/ cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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/ cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	5, Appl	, Appli	5, Appl	7, App	, Appl	95, Ap	87, App	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli
u :	m	e)	6	13	40	67	0	ý	9	ý	9	ý	ý	9	ý	9	9	7	7
Description	Sequence 36,	Sequence 3, Appl	Sequence 15, App.	Sequence 137,	Seguence 40,	Sednence 6795,	Sequence 787	Sequence 6,	Sednence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sednence	Sequence	Sequence
ΠD	US-09-839-447A-36	US-09-839-447A-3	US-10-105-929-15	US-09-759-130B-137	US-10-004-717-40	US-09-738-626-6795	US-09-925-297-787	US-09-992-598-6	US-09-989-293A-6	US-09-989-735-6	US-09-990-444-6	9-086-686-8n	US-09-990-436-6	US-09-991-181-6	US-09-993-687-6	US-09-989-734-6	US-09-997-653-6	US-10-174-590-2	US-10-176-758-2
98	10	10	12	6	6	6	10	σ	σ	6	6	δ	σ	6	0	σ	σ	σ	6
å Query Match Length DB	20	130	247	248	266	448	576	251	251	251	251	251	251	251	251	251	251	251	251
Query Match	88.0	88.0	74.0	74.0	74.0	70.0	70.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0
Score	44	44	37	37	37	35	35	34	34	34	34	34	34	34	34	34	34	34	34
Result No.	T	7	3	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19

Sequence 2, Appli Sequence 6, Appli		6, 0		7	7	7	ò	φÌ	9	ednence 6,	7	equence 2,	'n	7			'n	2,	7		Sequence 2, Appli	Sequence 2, Appli	
-10-175-737	US-10-173-706- US-10-175-738-	US-10-175-752-	US-10-176-482-	US-10-176-913-	US-10-180-552-	US-10-180-557-	US-09-990-438-	US-09-990-562-	US-09-997-428-	-999-266-60-sn	US-10-173-700-	US-10-174-572-	US-10-174-579-	US-10-174-582-	US-10-174-588-	US-10-175-739-	US-10-175-740-	US-10-175-743-	US-10-176-488-	US-10-176-492-	US-10-176-747-	US-10-176-750-	ALIGNMENTS
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20	22	24	25	27	28	29	0	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

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Gaps
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Sequence 36, Application US/09839447A

Sequence 36, Application US/09839447A

Sequence 36, Application US/09839447A

Sequence 36, Application US/09839447A

GENERAL INFORMATION:

APPLICANT: Sallberg, Matti

TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE

TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS

FILE REFERENCE: TRIPPE. 020CP1

CURRENT APPLICATION NUMBER: US/09/839,447A

CURRENT FILING DATE: 2001-08-09

PRIOR APPLICATION NUMBER: 09/556605

PRIOR PELING DATE: 2000-04-21

NUMBER OF SEQ ID NOS: 111

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.0%; Score 44; DB 10; Length 20; 88.9%; Pred. No. 0.096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09839447A
Patent No. US20020058247A1
GENERAL INFORMATION:
TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
TITLE OF INVENTION: HERATITIS B VIRUS CORE AND E ANTIGENS
FILE REFERENCE: TRIPEP. 0220CP1
CURRENT APPLICATION NUMBER: US/09/839,447A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Artificial Peptide US-09-839-447A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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US-09-839-447A-3
                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 36
LENGIH: 20
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: SOGHBI, HUDA Y.
APPLICANT: ZOGHBI, HUDA Y.
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEARNESS, TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION FILE REFERENCE: P01899US4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 9; Length 248;
Pred. No. 16;
0; Mismatches 1; Indels
                                                                                        TITLE REFERENCE: MOLES.
CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
FRIOR APPLICATION NUMBER: US 09/479,249
FRIOR PILING DATE: 2000-01-07
FRIOR PILING DATE: 2000-01-07
FRIOR APPLICATION NUMBER: US 09/559,497
FRIOR APPLICATION NUMBER: US 09/559,603
FRIOR APPLICATION NUMBER: US 09/578,063
FRIOR FILING DATE: 2000-05-24
FRIOR FILING DATE: 1999-06-14
FRIOR FILING DATE: 1999-06-14
FRIOR FILING DATE: 1999-06-14
FRIOR APPLICATION NUMBER: US 09/596,194
FRIOR FILING DATE: 1999-06-29
FRIOR APPLICATION NUMBER: US 09/608,452
FRIOR APPLICATION NUMBER: US 09/602,871
FRIOR APPLICATION NUMBER: US 09/602,871
FRIOR PRILING DATE: 1999-09-10
FRIOR FILING DATE: 2000-06-33
FRIOR APPLICATION NUMBER: US 09/420,707
FRIOR FILING DATE: 2000-06-33
FRIOR APPLICATION NUMBER: US 09/420,707
FRIOR FILING DATE: 2000-06-33
FRIOR FILING DATE: 2000-06-33
FRIOR FILING DATE: 2000-06-37
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CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/585,645
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 60/176,993
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 60/137,060
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 40
LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 137
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US-10-004-717-40
; Sequence 40, Application US/10004717
; Publication No. US20020192665Al
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Best Local Similarity 87.5%;
Matches 7; Conservative (
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Best Local Similarity
Tabas 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Rattus sp. US-09-759-130B-137
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Patent No. US20020137142a1

GENERAL INFORMATION:

APPLICANT: HOLTZMATION:

APPLICANT: HOLTZMATION:

TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83

FILE REFERENCE: 09404/041001,

CURRENT APPLICATION NUMBER: US/10/105,929

CURRENT PILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491

PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07

PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05

PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05

PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-05

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-05

SOUTWARE: FASTSEQ for WINGOWS Version 3.0

SEQ ID NO 15

LENGTH: 247
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                                                                                                                                                                                                                                                                                                                                                                                            88.0%; Score 44; DB 10; Length 130; 88.9%; Pred. No. 0.58;
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FUDLICATION No. US20030022279A1
GENERAL INFORMATION:
APPLICANT: MILLENDIUM Pharmaceuticals, Inc.
APPLICANT: MCCarthy, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
APPLICANT: Barnes, Thomas S
APPLICANT: Mist, Susan J
APPLICANT: Mackay, Charles R
APPLICANT: Mackay, Charles R
APPLICANT: Mackay, Charles R
APPLICANT: Leiby, Kevin R
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/556605
PRIOR FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Artificial Peptide
                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Goodearl, Andrew
Holtzman, Douglas A
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Best Local Similarity 88.99
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 RGKGTGFAY 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 GTGTGTAY 212
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PID20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065250
PRIOR PLING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-12
PRIOR PELLING DATE: 1997-11-12
PRIOR PELLING DATE: 1997-11-13
PRIOR PELLING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/06570
PRIOR PILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-02-25
PRIOR PAPLICATION NUMBER: 60/08332
PRIOR APPLICATION NUMBER: 60/08332
PRIOR APPLICATION NUMBER: 60/08332
PRIOR APPLICATION NUMBER: 60/08332
PRIOR APPLICATION NUMBER: 60/08760
PRIOR FILING DATE: 1998-05-28
PRIOR PELLING DATE: 1998-05-28
PRIOR PELLING DATE: 1998-05-28
PRIOR PELLING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR PELLING DATE: 1998-06-02
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PRIOR FILING DATE: 1998-06-02
PRIOR PPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
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PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
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                                                                                                                   Sequence 6, Application US/09992598 Patent No. US20020160384A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   Godowski, Paul J.
Grimaldi, J.Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                                                                                        Ferrara, Napoleone
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                                                                                                                                                                                                                                                                                                            Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                   Gurney, Austin L.
Kljavin, Ivar J.
                                                                                                                                                                              APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                               Baker, Kevin P.
Botstein, David
                                                                                                                                                                                                                                                                                                                                                  Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                         Napier, Mary A.
                                                                                                                                                                                                                                     Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumas, Daniel
                                                                                                                                                                                                                                                                                            Fong, Sherman
                  499 RGHGTGFCF 507
1 RGTGTGFAY 9
                                                                                       RESULT 8
US-09-992-598-6
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE PAJOS
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SEQ ID NO 787
LENGRH: Patentin Ver: 2.0
SEQ ID NO 787
LENGRH: 576
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Pred. No. 80;
1; Mismatches 2; Indels
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Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6795
                                                                                                                           ; Sequence 6795, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 787, Application US/09925297
Patent No. US20020081659A1
GENERAL INFORMATION:
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66.7%;
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ilarity 87.5%;
Conservative
                                                                                                                                                                                APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                   HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
                                                                                                                                                                                                                                                                                           TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 70.0 Best Local Similarity 66.7 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                IKEDA, MASATO
                                                                                                                                                                                                                  ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-297-787
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Best Local Similarity
7; Conserve
                      209 RGTGVGYPY 217
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386 RGTGTGAA 393
 1 RGTGTGFAY 9
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                                                                                                            US-09-738-626-6795
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APPLICANT:
APPLICANT:
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APPLICANT:
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PRIOR FILLING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089598
PRIOR APPLICATION NUMBER: 60/089599
PRIOR APPLICATION NUMBER: 60/089599
PRIOR PILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089601

PRIOR APPLICATION NUMBER: 60/089601

PRIOR PILING DATE: 1998-06-18

PRIOR PILING DATE: 1998-06-18

PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/089907

PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/089908

PRIOR APPLICATION NUMBER: 60/089908

PRIOR APPLICATION NUMBER: 60/089908

PRIOR APPLICATION NUMBER: 60/089947

PRIOR PILING DATE: 1998-06-19

PRIOR PILING DATE: 1998-06-19

PRIOR PILING DATE: 1998-06-19 APPLICATION NUMBER: 60/088028 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088029 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088030 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088202 FILING DATE: 1998-06-05 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088212 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088217 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09 APPLICATION NUMBER: 60/088734 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088738 APPLICATION NUMBER: 60/088033 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088326 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088742 FILING DATE: 1998-06-10 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089514 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/088167 60/088810 60/088824 APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088858 APPLICATION NUMBER: 60/088861 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876 APPLICATION NUMBER: 60/089105 FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/089440 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089512 APPLICATION NUMBER: 60/089532 60/089538 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090246 FILING DATE: 1998-06-10 FILING DATE: 1998-06-05 998-06-10 FILING DATE: 1998-06-10 FILING DATE: 1998-06-22 FILING DATE: 1998-06-11 FILING DATE: 1998-06-11 1998-06-1 APPLICATION NUMBER: FILING DATE: 1998-06 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1 PRIOR PRIOR

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PRIOR APPLICATION NUMBER: 60/090254
PRIOR PILING DATE: 1998-06-23
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PRIOR FILING DATE: 1998-06-24
PRIOR PAPLICATION NUMBER: 60/090439
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PRIOR PA APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 APPLICATION NUMBER: 60/091978 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-02 FILING DATE: 1998-07-07 Query Match Best Local Similarity '-hes 6; Conserva PRIOR PRIOR

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R APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/08861
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089952
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/088826
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089947
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088742
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FILING DATE: 1998-06-04
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               1998-06-04
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C66
FURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
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R APPLICATION NUMBER: 60/065186

R FILING DATE: 1997-11-12

R APPLICATION NUMBER: 60/065311

R FILING DATE: 1997-11-13

R FILING DATE: 1997-11-13
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R APPLICATION NUMBER: 60/084600
R APPLICATION NUMBER: 60/087106
R PILING DATE: 1998-05-28
R FILING DATE: 1998-05-28
R FILING DATE: 1998-06-02
R FILING DATE: 1998-06-02
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087759
APPLICATION NUMBER: 60/087827
APPLICATION NUMBER: 60/087827
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/078910
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                     Sequence 6, Application US/09989293A Patent No. US20020177164A1
                                                                                                                                                                                                                                                                                                                                                       Godowski, Paul J.
Grimaldi, J.Christopher
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Gerritsen, Mary E.
Goddard, Audrey
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                                                                                                                       Baker, Kevin P.
Botstein, David
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                                                                    GENERAL INFORMATION:
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US-09-989-293A-6
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/08910
PRIOR PILING DATE: 1998-02-25
PRIOR PELING DATE: 1998-02-25
PRIOR PELING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/08460
PRIOR PLING DATE: 1998-06-07
PRIOR PELING DATE: 1998-06-07
PRIOR APPLICATION NUMBER: 60/08760
PRIOR PELING DATE: 1998-06-07
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PRIOR PELING DATE: 1998-06-03
PRIOR PELING DATE: 1998-06-04
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Grimaldi, J. Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
                                                                   Ferrara, Napoleone
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Goddard, Audrey
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Pan, James
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                                                                                                 Fong, Sherman
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PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
PRIOR PELICATION NUMBER: 60/091478
PRIOR PELICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR APPLICATION NUMBER: 60/091638
PRIOR FILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
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PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090540
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/090690
FILING DATE: 1998-06-25
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090676
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APPLICATION NUMBER: 60/090557
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APPLICATION NUMBER: 60/090678
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APPLICATION UNMBER: 60/090863
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
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PRIOR FILING DATE: 1998-07-07
PRIOR PPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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65 GPGTGFLY 72
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FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/

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APPLICATION NUMBER: 60/088167 FILING DATE: 1998-06-05 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088202

Sequence 6, Application US/09989735
Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: AShkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David

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A APPLICATION NUMBER: 60/089948
R FILING DATE: 1998-06-19
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R FILING DATE: 1998-06-12
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R APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/090355
FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
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APPLICATION UNMBER: 60/089538
APLLING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/089653
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APPLICATION UNMBER: 60/089801
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/090254
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
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APPLICATION NUMBER: 60/088824
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088734
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-11
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Gaps ö 68.0%; Score 34; DB 9; Length 251; 75.0%; Pred. No. 53; Indels Mismatches PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090676
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PRIOR FILING DATE: 1998-06-25 PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 PRIOR APPLICATION NUMBER: 60/092182 PRIOR FILING DATE: 1998-07-09 APPLICATION NUMBER: 60/091360 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 PPLICATION NUMBER: 60/091544 FILING DATE: 1998-07-01 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091519 FILING DATE: 1998-07-02 PRIOR FILING DATE: 1998-07-02 PRIOR APPLICATION NUMBER: 60/091978 APPLICATION NUMBER: 60/090678 FILLING DATE: 1998-06-25 APPLICATION NUMBER: 60/090690 APPLICATION NUMBER: 60/090862 FILLING DATE: 1998-06-26 APPLICATION NUMBER: 60/090863 APPLICATION NUMBER: 60/091626 APPLICATION NUMBER: 60/091633 APPLICATION NUMBER: 60/090694 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090695 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090696 US-09-990-444-6
; Sequence 6, Application US/0990444
; Publication No. US20020193300Al
; GENERAL INPORMATION: PRIOR APPLICATION NUMBER: 60/090444 .. Desnoyers, Luc Eaton, Dan L. Ferrara, Napoleone 1998-06-26 1998-07-02 Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey FILING DATE: 1998-06-25 FILING DATE: 1998-06-25 APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P. Conservative Botstein, David Fong, Sherman Query Match Best Local Similarity Matches 6; Conserv | ||||| | 65 GPGTGFLY 72 FILING DATE: FILING DATE: 2 GTGTGFAY 9 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: RESULT 11 PRIOR õ

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APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10
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FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089512
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472
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FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089952
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090355
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APPLICATION UNMBER: 60/090431
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/090535
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FILING DATE: 1998-06-22
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CURRENT APPLICATION NUMBER: US/09/990,444
PRICA PAPLICATION NUMBER: 60/049787
PRICA PAPLICATION NUMBER: 60/049787
PRICA PAPLICATION NUMBER: 60/062250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/076945
PRIOR APPLICATION NUMBER: 60/078910
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-06-07
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PRIOR PELING DATE: 1998-06-02
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
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FILING DATE: 1998-06-03
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APPLICATION NUMBER: 60/088025
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088655
FILING DATE: 1998-06-09
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
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                       Grimaldi, J.Christopher
Gurney, Austin L.
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                                                                                                                                                                                                                    Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                         Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Godowski, Paul J.
                                                                        Kljavin, Ivar J.
                                                                                             Napier, Mary A.
                                                                                                                                                                                                                                                                                                                         Zhang, Zemin
                                                                                                                            Pan, James
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ATTLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same CURRENBACE: PAT30PTO69 CURRENT APPLICATION NUMBER: 05/09/989,730 CURRENT FILING DATE: 2001-11-20 PRIOR APPLICATION NUMBER: 60/049787 PRIOR PLICATION NUMBER: 60/049787 PRIOR PLICATION NUMBER: 60/049787 PRIOR APPLICATION NUMBER: 60/062250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/088217
PRIOR PELLING DATE: 1998-06-05
PRIOR PELLING DATE: 1998-06-05
PRIOR PELLING DATE: 1998-06-09
PRIOR PELLING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR PILING DATE: 1998-06-10
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PRIOR PELLING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/08810
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OR APPLICATION NUMBER: 60/088033
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OR APPLICATION NUMBER: 60/088326
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088167
OR FILING DATE: 1998-06-05
                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR PAPLICATION NUMBER: 60/065311
PRIOR PELING DATE: 1997-11-13
PRIOR PRILING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/079910
PRIOR PILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR PRILING DATE: 1998-03-20
PRIOR PRILING DATE: 1998-04-28
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217
APPLICATION NUMBER: 60/088655
APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/088029
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/088025
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APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088021
                                                                      Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
Roy, Margaret Ann
Stewart, Timothy A.
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                                                  Tumas, Daniel
                                                                                                                                              Zhang, Zemin
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Pred. No. 53;
0; Mismatches 2; Indels
                                                                                PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090676
PRIOR APPLICATION NUMBER: 60/090676
PRIOR APPLICATION NUMBER: 60/090678
PRIOR PILING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
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PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PILING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/090862
PRIOR PLING DATE: 1998-06-26
PRIOR PAPLICATION NUMBER: 60/090863
PRIOR PLING DATE: 1998-06-26
PRIOR PAPLICATION NUMBER: 60/091860
PRIOR PLING DATE: 1998-06-26
PRIOR PAPLICATION NUMBER: 60/091860
PRIOR PELING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/09154
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091638
PRIOR APPLICATION NUMBER: 60/091639
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Grimaldi, J.Christopher
Gurney, Austin L.
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               FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090540
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090542
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75.0%;
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Napier, Mary A.
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Matches 6; Conservative
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Botstein, David
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Eaton, Dan L.
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US-09-989-730-6
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Gaps ; 0 68.0%; Score 34; DB 9; Length 251; 75.0%; Pred. No. 53; Live 0; Mismatches 2; Indels PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR PILING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/090694
PRIOR PILING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/090695
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PRIOR PILING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/09063
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PRIOR PAPLICATION NUMBER: 60/090863
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PRIOR PELING DATE: 1998-07-01
PRIOR PAPLICATION NUMBER: 60/091478
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PRIOR PAPLICATION NUMBER: 60/091519
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APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09 Sequence 6, Application US/09990436 Publication No. US20020198148A1 Godowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L. Watanabe, Colin K. Williams, P. Mickey Wood, William I. Roy, Margaret Ann Stewart, Timothy A. Ferrara, Napoleone Gerritsen, Mary E. Goddard, Audrey Paoni, Nicholas F. Gerber, Hanspeter Best Local Similarity 75.0 Matches 6; Conservative APPLICANT: Ashkenazi, Avi J. Kljavin, Ivar J. Baker, Kevin P. Botstein, David Napler, Mary A. Desnoyers, Luc Tumas, Daniel Fong, Sherman Eaton, Dan L. GENERAL INFORMATION: | |||| | 65 GPGTGFLY 72 2 GTGTGFAY 9 US-09-990-436-6 Query Match APPLICANT: APPLICANT: APPLICANT: APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT δ

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R APPLICATION NUMBER: 60/090349
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R APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090694
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APPLICATION NUMBER: 60/089952
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APPLICATION NUMBER: 60/090254
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APPLICATION NUMBER: 60/089653
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APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/089801
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APPLICATION NUMBER: 60/088861
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   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 2001-11-14
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PRIOR APPLICATION NUMBER: 60/065186
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R FILING DATE: 1998-06-09
R APPLICATION NUMBER: 60/088734
R FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
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APPLICATION UNDBER: 60/088025
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APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/088824
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APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/087106
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827
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APPLICATION NUMBER: 60/088028
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APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088021
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PRIOR APPLICATION NUMBER: 60/08025
PRIOR FILING DATE: 1998-06-04
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PRIOR PELING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR PELING DATE: 1998-06-10
                                            PRILING DATE: 1997-10-17

R APPLICATION NUMBER: 60/065186

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PR APPLICATION NUMBER: 60/065311

R APPLICATION NUMBER: 60/065710

R APPLICATION NUMBER: 60/066770

PR FILING DATE: 1997-11-24

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APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/084600
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APPLICATION NUMBER: 60/087106
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APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088824
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APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIDC3
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CURRENT FILING DATE: 2001-11-16
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Publication No. US20020197615A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Grimaldi, J.Christopher
Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Paoni, Nicholas F.
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Eaton, Dan L.
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Best Local Similarity
Matches 6; Conserv
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65 GPGTGFLY 72
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US-09-991-181-6
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R APPLICATION NUMBER: 60/090535

OR FILING DATE: 1998-06-24

OR APPLICATION NUMBER: 60/090540

OR FILING DATE: 1998-06-24

OR APPLICATION NUMBER: 60/090542

OR FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/090435
R FILING DATE: 1998-06-24
R APLICATION NUMBER: 60/090444
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090445
R FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/090254
R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090349
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090355
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090429
               PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR PAPLICATION NUMBER: 60/089514
PRIOR PAPLICATION NUMBER: 60/089532
PRIOR APPLICATION NUMBER: 60/089538
PRIOR PAPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR PAPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR PAPLICATION NUMBER: 60/089609
PRIOR PILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089609
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089609
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089601
PRIOR APPLICATION NUMBER: 60/089601
PRIOR PRILING DATE: 1998-06-18
PRIOR PRILING DATE: 1998-06-18
PRIOR PAPLICATION NUMBER: 60/089901
PRIOR PELING DATE: 1998-06-18
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R APPLICATION NUMBER: 60/089801

R FILING DATE: 1998-06-18

R PELLING DATE: 1998-06-18

R APPLICATION NUMBER: 60/089907

R APPLICATION NUMBER: 60/089908

R APPLICATION NUMBER: 60/089908

R APPLICATION NUMBER: 60/089947

R APPLICATION NUMBER: 60/089947

R APPLICATION NUMBER: 60/089947

R APPLICATION NUMBER: 60/089948
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APPLICATION NUMBER: 60/090696
FILING DATE: 1998-06-25
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/089952
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090252
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FILING DATE: 1998-06-16
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C11
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CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PILING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
                                 PRIOR FILLING DATE: 1998-00-20
PRIOR FILLING DATE: 1998-00-01
PRIOR FILING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR PAPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-02
PRIOR PAPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-07
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Grimaldi, J. Christopher
Gurney, Austin L.
PRIOR APPLICATION NUMBER: 60/090863
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US-09-993-687-6
Sequence 6, Application US/09993687
Publication No. US20020198149A1
GENERAL INFORMATION:
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Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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                          FILING DATE: 1998-06-2
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Botstein, David
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Best Local Similarity
Matches 6; Conserv
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65 GPGTGFLY 72
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PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR PILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR PLING DATE: 1998-06-08
PRIOR PILING DATE: 1998-06-08
PRIOR PILING DATE: 1998-06-09
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR PELING DATE: 1998-06-02
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PRIOR PELING DATE: 1998-06-03
PRIOR PELING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR APPLICATION NUMBER: 60/088028
PRIOR PELING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/088028
PRIOR PELING DATE: 1998-06-04
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R APPLICATION NUMBER: 60/075945
R FILING DATE: 1998-02-25
R APPLICATION NUMBER: 60/078910
R FILING DATE: 1998-03-20
R APPLICATION NUMBER: 60/083322
R APPLICATION NUMBER: 60/083328
R APPLICATION NUMBER: 60/084600
R FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-06-06
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FILING DATE: 1998-06-10
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PRIOR FILING DATE: 1936-06-17
PRIOR PRILCATION NUMBER: 60/089653
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PRIOR FILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/090355
PRIOR PELING DATE: 1998-06-23
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PRIOR FILING DATE: 1998-06-18 R FILING DATE: 1998-06-23

R APPLICATION NUMBER: 60/090429

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090431

R APPLICATION NUMBER: 60/090435

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R FILING DATE: 1998-06-24

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PRIOR APPLICATION NUMBER: 60/090676
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PRIOR APPLICATION NUMBER: 60/090676
PRIOR APPLICATION NUMBER: 60/090690
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR PLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
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PRIOR APPLICATION NUMBER: 60/090695
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PRIOR APPLICATION NUMBER: 60/090695
PRIOR APPLICATION NUMBER: 60/090696 FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535 FILING DATE: 1998-06-24 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/090863 APPLICATION NUMBER: 60/091360 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/090862 APPLICATION NUMBER: 60/091544 FILING DATE: 1998-06-26 PRIOR PRIOR

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PRIOR FILING DATE: 1998-07-01
PRIOR PLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR PRIOR PAPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-07
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PRIOR P
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2 GTGTGFAY 9 | |||| | | 5 GPGTGFLY 72 Search completed: February 14, 2003, 11:21:30 Job time : 6.22581 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 14, 2003, 11:12:02; Search time 9 Seconds (without alignments) 96.134 Million cell updates/sec Run on:

US-09-701-001B-3 50 1 RGTGTGFAY 9 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues ched:

283224 Notal number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ption	probable lipoxygen	_	Ig mu chain C regi	androgen-withdrawa	hypothetical prote	rypeptidase	rab15 protein - wh	RAB21 protein - ri	probable dehydrin	carboxypeptidase C	probable MFS trans	probable carboxype	carboxypeptidase C	carboxypeptidase C	probable acriflavi	probable adhesin Y	conserved hypothet	hypothetical prote	serine proteinase		а	TXBP151 - human	ರ		capsid	cap	villin - chicken	-	hypothetical prote
ID	A83499	E84976	A45804	A39484	AE2040	T10856	S19130	S01152	T03392	A35275	A83383	T03607	A29412	S22530	н96007	AE0074	A89904	C95278	AD2451	AD1894	S77538	G02043	UMMS	VPXRPC	S45060	S45061	A31822	85	F82709
DB	2	7	7	7	7	7	7	7	7	Н	7	Н	Н	Н	7	7	~	7	7	7	7	7	Н	7	~	~	7	7	7
Length	685	483	568	280	502	101	149	163	165	411	423	429	499	200	1077	3295	163	398	401	429	452	563	713	736	744	744	826	1005	66
% Query Match	78.0	76.0	76.0	74.0	74.0		72.0	$^{\circ}$	72.0	72.0	72.0	72.0	72.0	72.0	72.0	72.0	70.0	70.0	70.0		70.0	70.0	70.0	70.0	70.0	70.0	70.0		68.0
Score	39	38	38	37	37	36	36	36	36	36	36	36	36	36	36	36	35	35	35	35	35	35	35	35	35	35	35	35	34
Result No.	1	7	m	4	20	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22 .	23	24	25	26	27	28	29

cytochrome c - Chl	hypothetical prote	ZC262.2 protein -	probable inositol	hypothetical prote	probable ribA prot	histidinol-phospha	amino acid ABC tra	hypothetical prote	probable sugar tra	MFS permease [impo	tubulin alpha chai	tubulin alpha chai	hypothetical prote	glycogen synthase	starch synthase (E
S29514	D70554	S44882	B87037	B84187	H70636	JQ0637	G82210	T47026	AG0235	AB2887	A56622	177426	C81701	B95130	00086н
H	7	7	~	~	7	-	7	7	7	7	7	7	~	7	7
112	216	233	291	305	353	369	401	409	409	449	450	450	462	477	477
68.0	68.0	0.89	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	0.89	68.0	68.0	68.0
34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34
30	31	32	۱ ۲	34	. K.	36	3.7	00	36	40	41	4.2	43	44	45

ALIGNMENTS

 RESULT 1 A83499 probable lipoxygenase PA1169 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginOsa C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C. ACCESSION: A03499 R.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; R.Strover, C.K.; Pham, X.O.; Erwin, A.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Ladman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337; PMID:10984043
 A; Accession: Accessio
 Query Match 78.0%; Score 39; DB 2; Length 685; Best Local Similarity 100.0%; Pred. No. 46; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy

tidD protein [imported] - Buchnera sp. (strain APS)

C;Species: Buchnera sp.
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: E84976
R;Shiqenobu, S; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp
A;Accession: E84976
A;Accession: E84976
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-483 cSTO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Residues: 1-483 cSTO>
A;Cross-references: strain APS
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: Escherichia coli tldD protein

76.0%; Score 38; DB 2; Length 483; 77.8%; Pred. No. 49; Query Match Best Local Similarity

Fri Feb 14 15:00:53 2003

RESULT 3

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Rikaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
BNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                     C.Species: Nostoc sp. A.Note: Nostoc sp. A.Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carboxypeptidase C (EC 3.4.16.5) - mung bean (fragment)
N.Alternate names: serine carboxypeptidase II
C.Species: Vigna raddata (mung bean)
C.Species: Vigna raddata (mung bean)
C.Species: 10-701-1999 #sequence_revision 16-701-1999 #text_change 08-Dec-2000
R.Stee, K. Tan "Allson, A.L.; Wilson, K.A.
Submitted to the EMBL Data Library, February 1996
A.Scession: T10856
A.Stetus: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-502 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73574.1; PID:g17130965; GSPDB:GN00179
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C:Species: Triticum aestivum (common wheat)
C:Decies: Triticum aestivum (common wheat)
C:Decies: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Aug-1999
C:Accession: S19130; S16758
R:King, S.W.; Joshi, C.P.; Nguyen, H.T.
Plant Mol. Biol. 18, 119-121, 1992
                                      Gaps
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                                   Indels
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Pred. No. 75;
                            Mismatches
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C, Genetics:
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77.8%;
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159 RGSGTGEAY 167
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                                                                                        2 GTGTGFAY 9
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                                                                                                                                                                                                                                                             A45804

Ig mu chain C region precursor, secreted form - channel catfish

(Species: Ictalurus punctatus (channel catfish)

(Species: 10-30-8ep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000

(Shacession: A45804; A30331; S12833

R.Ghaffari, S.H.: Lobb, C.J.

J. Immunol. 143, 2730-2739, 1989

A;Title: Nucleotide sequence of channel catfish heavy chain cDNA and genomic blot analys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 325-568 <GH2>
A; RCross-references: GB: M3733; NID:9213316; PIDN:AAA49329.1; PID:9213317
A; Residues: 325-568 <GH2>
A; Residues: 325-568 <GH2>
A; Rilson, M.R.; Marcuz, A.; van Ginkel, F.; Miller, N.W.; Clem, L.W.; Middleton, D.; War Nucleic Acids Res. 18, 5227-5233, 1990
A; Title: The immunoglobulin M heavy chain constant region gene of the channel catfish, I A; Reference number: S12833; MUD:90384824; PMID:2119496
A; Reference number: S12833
A; Molecule type: DNA
A; Residues: 135-568 <WIL>
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: alternative splicing; heterotetramer; immunoglobulin
C; Superfamily: sequence #status predicted <SIG>
F; 1-17/Domain: signal sequence #status predicted <SIG>
F; 18-568/Product: Ig mu chain C region, secreted form #status predicted <MAT>
F; 31-113/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haffari, S.H.; Lobb, C.J.
J. Immunol. 142, 1356-1365, 1989
A; Ithe: Cloning and sequence analysis of channel catfish heavy chain cDNA indicate phyl
A; Reference number: A30331; MUID:89124381; PMID:2492581
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R; Briehl, M.M.; Miesfeld, R.L.
Nol. Endocrinol. 5, 1381-1388, 1991
A; Fitle: Isolation and characterization of transcripts induced by androgen withdrawal an A; Reference number: A39484 MUID:92130987; PMID:1723140
A; Reference number: A39484
A; Molecule type: mRNA
A; Residues: 1-280 < BRI>
A; Cross-references: GB:M74067; NID:9205857; PIDN:AAA41760.1; PID:9205858
C; Genetics:
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C;Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 04-Mar-2000
          Gaps
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.oss-references: GB:M27230; NID:9213318; PIDN:AAA79003.1; PID:9213319
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              Indels
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C;Superfamily: rat androgen-withdrawal apoptosis protein RVP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  androgen-withdrawal apoptosis protein RVP1, prostatic - rat
          2;
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57;
       Mismatches
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   0;
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87.5%;
   Conservative
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les 7; Conserv
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Best Local Similarity
                                                                                                         72 RGESTGFAY 80
                                                               1 RGTGTGFAY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary A; Molecule type: mRNA
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70 GTGTGFA 76
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Matches
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Matches

RESULT 4

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Nalternate names: carboxypeptidase III
C;Species: Hordeum vulgare (parley)
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999
C;Accession: A35275
C;Accession: A35275; MUD:90315015; PMID:2639682
A;Title: Primary structure of carboxypeptidase III from malted barley.
A;Reference number: A35275; MUD:90315015; PMID:2639682
A;Reference number: A35275
A;Note: 185-Val was also found
C;Superfamily: serine carboxypeptidase
C;Keywords: blocked amino end; glycoprotein; hydrolase; serine carboxypeptidase
C;Keywords: blocked amino end; (Leu) (probably acetylated) #status experimental
F;17/Muding site: carbohydrate (Asn) (covalent) #status experimental
F;143,331,388/Active site: Ser, Asp, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable MFS transporter PA2114 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; vuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reducis: preliminary
A;Molecule type: DNA
A;Residues: 1-423 <STO>
A;Cross-references: GB:AE004638; GB:AE004091; NID:g9948116; PIDN:AAG05502.1; GSPDB:GN
C;Genetics:
A;Gene: PA114
A;Gene: PA114
A;Gene: PA114
A;Gene: PA114
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N;Alternate names: serine-type carboxypeptidase homolog
C;Species: Oryza sativa (rice)
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 21-Jul-2000
C;Accession: T03607
R; Ishkaway, K.
Plant Physiol. 105, 1275-1280, 1994
A;Title: Organ-specific and hormone-dependent expression of genes for serine carboxyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.0%; Score 36; DB 66.7%; Pred. No. 94; Live 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.0%; Score 36; DB ilarity 85.7%; Pred. No. 92; Conservative 1; Mismatches
                                                                                                                 carboxypeptidase C (EC 3.4.16.5) - barley
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Best Local Similarity 66.7
Matches 6; Conservative
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Matches 6; Conserv
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94 TGTGFSY 100
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A;Title: DNA sequence of an ABA-responsive gene (rab 15) from water-stressed wheat roots A;Reference number: S19130; MUID:92119217; PMID:1531029
A;Accession: S19130
A;Molecule type: mRNA
A;Residues: 1-149 <KIN>
A;Cross-references: EMBL:X59133; NID:921850; PIDN:CAA41850.1; PID:921851
C;Genetics:
C;Genetics:
C;Superfamily: dehydrin-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAB21 protein - rice
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1990 #text_change 20-Aug-1999
C;Accession: S01152
R;Mundy, J.; Chua, N. H.
EMBO J. 7, 279-2286, 1988
A;Title: Abscisic acid and water-stress induce the expression of a novel rice gene.
A;Reference number: S01152; MUID:89052639; PMID:2973410
A;Recion: S01152
A;Molecule type: DNA
A;Residues: 1-163 < MUNA
A;Residues: 1-163 < MUNA
A;Cross-references: EMBL:Y00842; NID:q20316; PIDN:CAA68765.1; PID:q295826
A;Note: the authors translated the codon GCG for residue 28 as Gly
C;Genetics:
A;Gene: RAB21
A;Introns: 70/3
C;Superfamily: dehydrin-like protein
C;Keywords: seed
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C;Superfamily: dehydrin-like protein
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Aug-1999
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R; McEvoy, S. M.; Sheoran, I.S.; Saini, H.S.
submitted to the EMBL Data Library, June 1996
A; Description: A rice CDNA encoding a late embryogenesis abundant protein.
A; Reference number: Z14923
A; Accession: T03392
A; Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 34;
0; Mismatches 1; Indels
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Pred. No. 38;
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0; Mismatches
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87.5%;
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87.5%;
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Local Similarity 87.5%;
hes 7; Conservative
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Best Local Similarity 87.5.
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A; Residues: 1-165 <MCE>
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T03392
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A;Gene: acrF; SMb21498
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| 673 GTGSGFEY 680
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A29412
carboxypeptidase C (EC 3.4.16.5) precursor - wheat
N;Alternate names: carboxypeptidase Y homolog
C;Species: Triticum aestivum (common wheat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Nov-1999
C;Accession: A29412
J Biol. Chem. 262, 1376-1375, 1987
A;Title: A gibberellin responsive wheat gene has homology to yeast carboxypeptidase Y. A;Reference number: A29412; MUID:88007602; PMID:2820978
A;Reference number: A29412; MUID:88007602; PMID:2820978
A;Reference number: A29412; MUID:88007602; PMID:2820978
A;Residues: 1-499 < CAUJOROT C: CAUJOR
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N.Alternate names: carboxypeptidase III
N.Alternate names: carboxypeptidase III
C.Specias: Oryza sativa (rice)
C.Specias: Oryza sativa (rice)
C.Specias: Oryza sativa (rice)
C.Specias: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Nov-1999
C.Accession: $2253
C.Accession: 19, 640, 1992
A.Title: Structure and expression during the germination of rice seeds of the gene for A.Reference number: $22530; MUID:92329723; PMID:1627776
A.Accession: $22530
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A; Reference number: 214975; MUID:95062718; PMID:7972496
A; Accession: T03607
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-429 <WAS>
A; Cross references: EMBL:D17887; NID:9409581; PIDN:BAA04511.1; PID:9409582
A; Experimental source: cv. Yukihikari
C; Genetics:
A; Genetic
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A; Cross-references: EMBL: S40458
Genetics:
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Matches 6; Conserv
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tches 6; Conserv
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167 TGTGFSY 173
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probable acriflavin resistence protein [imported] - Sinorhizobium meliloti (strain 10 c; Species: Sinorhizobium meliloti (c; Species: Spec
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A, Molecule Trype: DNA
A, Residues: 1-1077 < KURN>
A, Cross-references: GB:AL591985, PIDN:CAC49728.1; PID:g15141215; GSPDB:GN00167
A, Experimental source: strain 1021, megaplasmid pSymb
R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
D:, Hyman, R.W.; Jones, T.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
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A; Reference number: A96039; MUID:21368234; PMID:11474104
A; Contents: annotation
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A;Introns: 100/2; 156/3; 196/3; 244/3; 295/1; 324/3; 411/1; 455/3
C;Superfamily: serine carboxypeptidase
C;Keywords: glycoprotein; hydrolase; serine carboxypeptidase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-73/Domain: propeptide #status predicted <PRO>
F;74-484/Product: carboxypeptidase C #status predicted <NAT>
F;485-499/Domain: carboxyl-terminal propeptide #status predicted 
F;14/Abinding site: carboxyl-terminal propeptide #status predicted
F;216,404,461/Active site: Ser, Asp, His #status predicted
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Pred. No. 1.18+02;
1; Mismatches 0;
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C;Superfamily: acriflavin resistance protein
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85.7%;
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Best Local Similarity
6; Conserva
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Compugen Ltd.
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compug
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- protein search, using sw model OM protein February 14, 2003, 11:05:27; Search time 4.64516 Seconds (without alignments) 80.360 Million cell updates/sec Run on:

US-09-701-001B-3 50 Perfect score:

1 RGTGTGFAY 9

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues ched:

cal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	7.50 7.50 7.50 7.50 7.50 7.50 7.50 7.50	1 !	 TLDD_BUCAI CLD3_MOUSE CLD3_RAT DH12_WHEAT DH12_WHEAT DH12_WHEAT CBP3_CRYSA CBP3_CRYSA CBP3_CRYSA CBP3_CRYSA CBP3_CRYSA CBP3_CRYSA CBP3_CRYSA CBP3_CRYSA VILI_CHICK CYC_CHLRE VOLC_CEEL CODS_CALCK SUHB_MYCLE HIBL_STRCO HIBL_STRCO TBA2_HUMAN TBA3_MOUSE TBA2_HUMAN TBA3_MOUSE TBA2_HOMAN TBA3_MOUSE TBA2_HOMAN TBA3_HOMAN	P57478 buchnera ap Q57478 buchnera ap Q5209 mus musculu Q63400 rattus norv Q00742 triticum ae P12253 oryza sativ P52712 oryza sativ P51512 brordeum vul P1515 triticum ae P21529 hordeum vul P26193 porcine rot P02640 gallus gall P15451 chlamydomon P3454 caenorhabdi Q42398 gallus gall P46813 mycobacteri P16246 streptonyce P55427 rhizobium s Q13748 homo sapien P08214 mus musculu P18280 oncorhynchu Q94570 homarus ame Q94570 homarus
322 332 332 332 332	1 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6		940 905 1394 1401 1415 157 356 385 405	 YOAA HAEIN HAP HAEIN RPOC_VIBCH RPOC_LABIN Y188_RICPR PROB_AQUAE ARGD_BACSU XJHB ECOLI	P44680 naemophilus Q10860 mycobacteri P45387 haemophilus Q9kv29 vibrio chol P43739 haemophilus Q9zdx6 ricketteia Q67209 aquifex aeo P36839 bacillus su P39352 escherichia P30145 bacillus ps

P12581 influenza a	Q9jw13 neisseria m	Q9jxv7 neisseria m	O70141 rattus norv	Q01107 bos taurus	Q04861 gallus gall	Q9xyc2 orconectes	P32718 escherichia	Q9sel7 arabidopsis	Q59678 pasteurella	P55180 bacillus su	P18645 rattus norv
HEMA_IACKG	DXS_NEIMA	DXS_NEIMB	SM6B_RAT	DSC1_BOVIN	KBF1_CHICK	RL15_ORCLI	ALSK_ECOLI	HHOA_ARATH	GALE_PASHA	GALE_BACSU	GALE_RAT
Н	-	-	Н	Н	Н	Н	-	Н	Н	Н	Н
561	637	637	887	893	984	204	309	321	338	339	347
0.99	0.99	0.99	0.99	0.99	0.99	64.0	64.0	64.0	64.0	64.0	64.0
33	33	33	33	33	33	32	32	32	32	32	32
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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                                                                                                                                                                                                Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20445173; PubMed=10993077; Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.; Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.; "Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS."; Nature 407:81-86(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLD3_MOUSE STANDARD; PRT; 219 AA.
CLD3_MOUSE STANDARD;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2012 (Rel. 41, Last annotation update)
16-JUN-2012 (Rel. 41, Last annotation update)
17-JUN-2012 (Rel. 41, Last annotation update)
18-JUN-2012 (Rel. 41, Last annotation update)
18-JUN-2012 (Rel. 41, Last annotation update)
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Pred. No. 25;
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                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17IdD protein homolog.
17DD OR BU398.
                        483 AA.
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InterPro; IPR002510; PmbA_TldD.
Pfam; PF01523; PmbA_TldD; 1.
Complete Protecome.
SEQUENCE 483 AA; 52977 MW; 1
                                                                     16-OCT-2001 (Rel. 40, Created)
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Best Local Similarity 77.8
Matches 7; Conservative
                        STANDARD;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-TOkyo 1998;
                                                                                                                                                                                                                                                                             NCBI_TaxID=118099;
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                          TLDD_BUCAI
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TLDD_BUCAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                         Paperna T., Peoples R., Wang Y.K., Kaplan P., Francke U.;
"Genes for the CPE receptor (CPETR1) and the human homolog of RVP1
(CPETR2) are localized within the Williams-Beuren syndrome deletion.";
Genomics 54:453-459(1998).
                                                                                                                                                                                                                                                   Morita K., Furuse M., Fujimoto K., Tsukita S.;
"Claudin multigene family encoding four-transmembrane domain protein
components of tight junction strands ";
Proc. Natl. Acad. Sci. U.S.A. 96:511-516(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                           Strausberg R;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF095905; AAD14608.1; -.
EMBL; AF087821; AAD09756.1; -.
EMBL; BC012650, AAH12650.1; -.
MGD; MGI:1329044; Claudin.
InterPro; IPR001832; Claudin.
Pfam; PF00822; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin.
PRINTS; PR01077; CLAUDIN.
PROSITE; PS01346; CLAUDIN.
ITGHT Junction; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING (IN ISOFORM 2).
62F67810D9B9BD37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       produced by alternative splicing.
-!- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Claudin-3 (Ventral prostate.1 protein) (RVP1).
CLDN3.
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87.5%; Pred. No. 1
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                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=99097345; Pubmed=9878248;
                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=99110921; PubMed=9892664;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 AA; 23284 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
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136
180
musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 7; Conserv
                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                              TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLD3_RAT
Q63400;
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CLD3_RAT
ID CLD3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G -> S (IN REF. 1).
MISSING (IN REF. 1).
DYV -> TTSERPGARTPHHHHYQPSMYPTRPACSLASETT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPSRRLQTPRSLLARLEEDRQPGVPFSPVAT (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.
                                                                                                           "Isolation and characterization of transcripts induced by androgen withdrawal and apoptotic cell death in the rat ventral prostate."; Mol. Endocrinol. 5:1381-1388(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 1; Length 219;
Pred. No. 18;
                                                                                                                                                                                      Keen T.J., Inglehearn C.F.,
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-I- SUBCELLULAR LOCATION: Integral membrane protein.
-I- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    820CC6BFC20D122D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M74067; AAA41760.1; -.
EMBL; AA011656; CAA09727.1; -.
INTERPO; IPR001832; Claudin.
INTERPO; IPR04031; PMP22_Claudin.
PRINTS; PR00422; PMP22_Claudin.
PRINTS; PR01077; CLAUDIN.
PROSITE; PS01346; CLAUDIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV. TAM W-101; TISSUE-ROOL;
MEDLINE-92119217; PubMed-1531029;
King S.W., Joshi C.P., Nguyen H.T.;
                                                                          MEDLINE=92130987; PubMed=1723140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tight junction; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23314 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.0%;
87.5%;
                                                                                              Briehl M.M., Miesfeld R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticum aestivum (Wheat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29
101
136
182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                             SEQUENCE FROM N.A.
                                                                                                                                                           [2]
SEQUENCE FROM N.A.
                               NCBI_TaxID=10116;
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28 96 140

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Seed; Seed embryo; Repeat.
63 71 POLY-SER.
PROSITE; PS00823; DEHYDRIN_2; 2
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ACT_SITE
                Dehydrin;
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REPEAT
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REPEAT
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                                                                                                                               Matches
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                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Abscisic acid and water-stress induce the expression of a novel rice
                                                                                                                                                                                                                                                                                                                         Gaps
    'DNA sequence of an ABA-responsive gene (rab 15) from water-stressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                               Score 36; DB 1; Length 149; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72183F7A99E467B1 CRC64;
                  wheat roots.";
plant Mol. Biol. 18:119-121(1992).
-i- INDUCTION: BY ABSCISIC ACID AND WATER STRESS.
-i- SIMILARITY: BELONGS TO THE PLANT DEHYDRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1989 (Rel. 12, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                163 AA
                                                                                                                                                                                                                                                                                                            pred. No. 18;
0; Mismatches
                                                                                                                                                                                                                                                                  POLY - SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Water-stress inducible protein RAB21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Indica-IR36; TISSUE-Seed; MEDLINE-89052639; PubMed-2973410; Mundy J.W., Chua N.-H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S01152; S01152.
InterPro; IPRO00167; Dehydrin.
Pfam; PF00257; dehydrin; 1.
PROSITE; PS00315; DEHYDRIN_1; 1.
                                                                                                                                                                                                      InterPro IPR000167; Dehydrin.
Pfam, PF00257; dehydrin; 1.
PROSITE; PS00315; DEHYDRIN_1; 1.
PROSITE; PS00823; DEHYDRIN_2; 2.
                                                                                                                                                                                                                                                                            SEQUENCE 149 AA; 15766 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y00842; CAA68765.1; -.
                                                                                                                                                                                                                                                                                                   72.0%;
87.5%;
                                                                                                                                                                      EMBL; X59133; CAA41850.1; -.
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                   PIR; S16758; S16758.
PIR; S19130; S19130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                             Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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P12253;
                                                                                                                                                                                                                                                       Dehydrin.
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Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
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SUBSTRATE (BY SIMILARITY).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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N-LINKED (GLCNAC. ..) (POTENTIAL).
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SIGNAL
SIGNAL
7 429 SERINE CARBOXYPEPTIDASE-LIKE.
CHAIN
ACT_SITE 148 148 BY SIMILARITY.
ACT_SITE 336 336 BY SIMILARITY.
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48;
                                                                                                          Length 163;
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96 TYPE B.
140 TYPE A.
1163 TYPE A.
16543 MW: 47FEDAD256DE7ACF CRC64;
                                                                                                                                                                                                                                                                                                                                                             CBPX_ORYSA STANDARD; PRT; 429 AA. P52712; 01-007-1996 (Rel. 34, Created) 10-007-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) serine carboxypeptidase-like precursor (EC 3.4.16.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARÎTY: BELONGS TO PEPTIDASE FAMILY S10.
                                                                                                          DB 1;
20;
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BY SIMILARITY.
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                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                            Score 36;
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Interpro; IPR001563; Serine_carbpept.
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                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                      Pred.
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85.7%;
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                                                                                                              72.0%;
87.5%;
                                                                                                                                                         Conservative
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Washio K., Ishikawa K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       broad specificity
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                                                                  163 AA;
                                                                                                                                 Local Similarity
nes 7; Conserv
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                                                                                                                                                                                                                                                   114 GTGTGGAY 121
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414
417
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167 TGTGFSY 173

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CBP3_WHEAT

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0
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CV. Yukihikari; TISSUE=Seed;
MEDLINE=92329723; PubMed=1627776;
Washio K., Ishikawa K.;
"Structure and expression during the germination of rice seeds of the
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: MONOMER (PROBABLE).
-!- INDUCTION: BY GIBBERELLIC ACID (GA). INHIBITED BY ABSCISIC ACID
                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                   gene for a carboxypeptidase.";
Plant Mol. Biol. 19:631-640(1992).
-1- CATALYTIC ACTIVITY: Release of a C-terminal amino acid with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL). AE455E2780147DB8 CRC64;
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PROSTRE; PS00131; CARBOXYPEPT_SER_SER; 1.
PROSITE; PS00560; CARBOXYPEPT_SER_HIS; 1.
Hydrolase; Carboxypeptidase; Glycoprotein; Zymogen; Signal.
SIGNAL 1 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
SERINE CARBOXYPEPTIDASE III.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
SY SUMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                    Spermātophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 500;
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                          01-0CT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine carboxypeptidase III precursor (EC 3.4.16.5).
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10.
                                                                                                                                     500 AA.
 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 56;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000379; Ser_estrs_site.
InterPro; IPR001563; Serine_carbpept.
                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00450; serine_carbpept; 1. PRINTS; PR00724; CRBOXYPTASEC.
                                                                                                                                                              01-OCT-1994 (Rel. 30, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55446 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D10985; BAA01757.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.73
6; Conservative
                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  broad specificity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S22530; S22530.
                                                                                                                                                                                                                                       Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lysc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500 AA;
                                                        99 TGTGFSY 105
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S10.009;
                             TGTGFAY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P00729;
                                                                                                                                     CBP3_ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                P37891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROPEP
                                                                                                                     CBP3_ORYSA
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
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                                                                                                     RESULT 7
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                                                                                                                             Spermātophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.
                                                                                                Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
                                                                                                                                                                                                                                                          J. Biol. Chem. 262:13726-13735(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó:
                                        01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine carboxypeptidase III precursor (EC 3.4.16.5) (CP-WIII).
                                                                                                                                                                                                                Baulcombe D.C., Barker R.F., Jarvis M.G.; "A gibberellin responsive wheat gene has homology to yeast carboxypeptidase Y.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SERINE CARBONYPEPTIDASE III.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
SUBSTRATE (BY SIMILARITY).
N'LINKED (GLCNAC. . .) (POTENT)
W, B2ACELOEF8484CDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Carboxypeptidase; Glycoprotein; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                               -i- INDUCTION: BY GIBBERELLIC ACID (GA).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10.
   500 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     508 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD001189; Serine_carbpept; 1.
PROSITE; PS00131; CARBOXYPEPT_SER_SER; 1.
PROSITE; PS00560; CARBOXYPEPT_SER_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.0%; Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000379; Ser_estrs_site.
InterPro; IPR001563; Serine_carbpept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00450; serine_carbpept; 1.
                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=88007602; PubMed=2820978;
                                                                                                                                                                                                                                                                                      broad specificity.
-!- SUBUNIT: MONOMER (PROBABLE)
                           01-OCT-1989 (Rel. 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00724; CRBOXYPTASEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55334 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J02817; AAA34273.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.78;
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73
484
500
216
404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A29412; A29412.
HSSP; P00729; 1CPY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             500 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                       NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; S10.009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 TGTGFSY 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 TGTGFAY 9
CBP3 WHEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBP3_HORVU
ID CBP3_HORVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
             P11515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROPEP
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Gaps

3 TGTGFAY 9

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174 TGTGFSY 180

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE: EXPRESSED MAINLY IN THE ALEURONE AND, TO A LESSER EXTENT IN THE EMBRYO, THROGHOUT THE 5-DAYS GERMINATION PERIOD EXCLUSIVELY, WHITH A MAXIMAL LEVEL AT 3 DAYS. ALSO FOUND IN THE ROOTS AND SHOOTS OF THE GROWING SEEDLING.
                                                                                              Hordeum vulgare (Barley).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                            STRAIN=CV. Gula;
MEDLINE=99315015; PubMed=2639682;
Soeronsen S.B., Svendsen I., Breddam K.;
Soeronsen S.B., Svendsen Ell from malted barley.";
Carlabberg Res. Commun. 54:193-202(1989).
-:- CATALYTIC ACTIVITY: Release of a C-terminal amino acid with a
P21529;
01-MAY-1991 (Rel. 18, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine_carboxypeptidase III precursor (EC 3.4.16.5) (CP-MIII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS, PRO0450; Serine_carbpept; 1.
PRINTS, PR00724; CRBOXYPTASEC.
ProDom; PR001189; Serine_carbpept; 1.
PROSITE; PS001019; CARBOXYPEPT_SER_SER; 1.
PROSITE; PS00560; CARBOXYPEPT_SER_HIS; 1.
HydroLase; Carboxypeptidase; Glycoprotein; Zymogen; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SERINE CARBOXYPEPTIDASE III
                                                                                                                                                                                                            STRAIN-cv. Himalaya; TISSUB-Aleurone;
Rocher A., Lok F., Cameron-Mills V., von Wettstein D.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> V (POLYMORPHISM).
70C6751D78D40AB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: SECRETED INTO THE ENDOSPERM.
                                                                                                                                                                                                                                                                                                                                                                                              broad specificity.
-!- ENZYME REGULATION: INHIBITED BY MERCURIC IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
SUBSTRATE.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000379; Ser_estrs_site.
InterPro; IPR001563; Serine_carbpept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOCKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56362 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y09604; CAA70817.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4491
508
81
223
4411
4414
414
151
265
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265
508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P00729; 1CPY.
MEROPS; $10.009; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                SEQUENCE OF 81-491.
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=4513;
                                                                                  CBP3 OR CXP; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                         DR
DR
DR
ETT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92124743; PubMed=1310192; Bremont M., Juste-Lesage P., Chabanne-Vautherot D., Charplidenne A., Cohen J.; Chaptilienne A., Cohen J.; Sequences of the four larger proteins of a porcine group C rotavirus and comparison with the equivalent group A rotavirus proteins.";
                                                                                                                                                                                                                                                                      Shin H.S., Bargiello T.A., Clark B.T., Jackson F.R., Young M.W.; "An unusual coding sequence from a Drosophila clock gene is conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rol. 22, Last sequence update)
01-MAY-1992 (Rel. 40, Last annotation update)
00ter capsid protein VP4 (Hemagajutinin) (Outer layer protein VP4)
[Contains: Outer capsid proteins VP5 and VP8].
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 1; Length 672;
Pred. No. 1.1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                            -! - SIMILARITY: TO OTHER G-T STRETCH CONTAINING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               672 AA; 57924 MW; E85BF428CF424C0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Porcine rotavirus (group C / strain Cowden).
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=10916;
                                                   01-AUG-1988 (Rel. 08, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Per-hexamer repeat protein 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    736 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-T REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M12039; AAA88320.1; -.
EMBL; X02966; CAA26710.1; ALT_INIT.
               PRT;
                                                                                                                                                                                                                                                      MEDLINE=86014384; PubMed=2413365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:104521; Phxr5.
InterPro; IPR000561; EGF-like.
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                               Nature 317:445-448(1985)
                   STANDARD;
                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
Les 7; Conserv
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              625 RGTGTGTA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGTGTGFA 8
                                                                                                                                                                                                                                                                                                            in vertebrates
                                                                                                                            PHXR5 OR PER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A24403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VP4_ROTPC
P26193;
                     PHX5_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
PHX5_MOUSE
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Pred. No. 56; 1; Mismatches

Conservative

Matches

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REPEAT
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                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-88276884; PubMed-2839826;
MEDLINE-88276884: Wallek M., Smeal T., Jakes R., Ahmed Y.;
"Villin sequence and peptide map identify six homologous domains.";
Proc. Natl. Acad. Sci. U.S.A. 85:4986-4990(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OUTER CAPSID PROTEIN VP4.
OUTER CAPSID PROTEIN VP8 (POTENTIAL).
OUTER CAPSID PROTEIN VP5 (POTENTIAL).
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D (GLCNAC...) (POTENTIAL).
D (GLCNAC...) (POTENTIAL).
Virology 186:684-692(1992).
-!- SUBCELLULAR LOCATION: Outer capsid.
-!- PTM: VPB IS ONE OF TWO TRYPSIN CLEAVAGE PRODUCTS OF VP4; THE OTHER PRODUCT IS VP5.
-!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-81264203; PubMed-6790532; Glenney J.R. Jr., Geisler N., Kaulfus P., Weber K.; Demonstration of at least two different actin-binding sites in villin, a calcium-regulated modulator of F-actin organization."; J. Biol. Chem. 256:8156-8161(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC. .) (POIDM....
(GLCNAC. .) (POIDMINIAL)
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85.7%; Pred. No. 1.2e+02;
ive 1; Mismatches 0; Indels
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01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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MEDLINE=83082892; PubMed=6848508;
                                                                                                                                                                                                                                                                                                                                                                                                                PIR; D40822; VPXRPC.....
InterPro: IPR000416; Cap_VP4.
Pfam: PF00426; VP4: 1
Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83231 MW;
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M74218; AAB00802.1; -.
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736 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                               Markus M.A., Matsudaira P., Wagner G.;
"Refined structure of villin 14T and a detailed comparison with other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GELSOLIN-LIKE 1.
GELSOLIN-LIKE 2.
GELSOLIN-LIKE 3.
GELSOLIN-LIKE 4.
GELSOLIN-LIKE 5.
GELSOLIN-LIKE 5.
GELSOLIN-LIKE 5.
CELSOLIN-LIKE 6.
ABSOLUTELY REQUIRED FOR ACTIVITY.
CRUCIAL FOR BINDING AN ACTIN FILAMENT.
POLYPHOSPHOINOSITIDE BINDING (BY
                                                                                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                              Markus M.A., Nakayama T., Matsudaira P., Wagner G.,
"Solution structure of villin 14T, a domain conserved among actin-
Hesterberg L.K., Weber K.; "Demonstration of three distinct calcium-binding sites in villin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoskeleton; Calcium; Actin-binding; Capping protein; Repeat; 3D-structure.
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POLYPHOSPHOINOSITIDE BINDING (BY SIMILARITY).
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                                                                                                       STRUCTURE BY NMR OF 1-127.
MEDLINE-94191534; PubMed-8142900;
                                                                                                                                                                                                                                                     STRUCTURE BY NMR OF 1-127.
MEDLINE=97337440; PubMed=9194180;
                                           modulator of actin assembly.";
J. Biol. Chem. 258:365-369(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, J03781; AAA49133.1; --
PIR; AA3082; A03082.
PIR; AA31822; A31822.
PDB; 2VIK, 01-APR-97.
PDB; 2VIL; 01-APR-97.
PDB; 1VIL; 12-AUG-97.
INTERPO; IPRO01974; Gelsolin.
INTERPO; IPRO01974; Gelsolin.
Pfam; PF00626; Gelsolin; 6.
Pfam; PF00209; WHP; 1.
PRINTS; PRO0209; GELSOLIN.
SMART; SMO0262; GEL; 6.
SMART; SMO0153; VHP; 1.
                                                                                                                                                                                                                                                                                                                                       actin-severing domains.";
Protein Sci. 6:1197-1209(1997).
                                                                                                                                                                                          severing proteins.";
Protein Sci. 3:70-81(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson R., Ainscough R., Adderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Calladhan M.,
Parsons J., Percy C., Rifken L., Roppra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Materston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                Mitochondrion; Electron transport; Respiratory chain; Heme
                                                                                                                                                                                                                               Score 34; DB 1; Length 111;
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 26.8 kDa protein 2C262.2 in chromosome III. 2C262.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 233 AA; 26825 MW; 84F99FB67A6DD5D6 CRC64;
                                                                                                                                                              IRON (HEME AXIAL LIGAND).
IRON (HEME AXIAL LIGAND).
6F11A35EA71C7078 CRC64;
                                                                                                                                  HEME (COVALENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                      233 AA.
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0; Mismatches
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                                                               ProDom; PD000375; Cyt_CIAB; 1.
PROSITE; PS00190; CYTOCHROME_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                  HEME
               Interpro; IPR002327; Cyt_CIAB. Pfam; PF00034; cytochrome_c; 1. PRINTS; PR00604; CYTCHRMECIAB.
                                                                                                                                                                                                 111 AA; 11826 MW;
InterPro; IPR003088; Cyt_CI.
InterPro; IPR002327; Cyt_CIAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L23647; AAK29991.1; -.
                                                                                                                                                                                                                                   68.0%;
75.0%;
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WormPep; ZC262.2; CE00350.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                    49 GTAAGFAY 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                    2 GTGTGFAY 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRINTIA 3.7. (C.125;
FRINTIA 3.8. (C.1997) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Blectron carrier protein. The oxidized form of the
cytochrome c heme group can accept an electron from the heme group
of the cytochrome c1 subunit of cytochrome reductase. Cytochrome of
then transfers this electron to the cytochrome oxidase complex,
the final protein carrier in the mitochondrial electron-transport
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=137c / CC-125, and cw15;
MEDLINE=89178731; PubMed=2853233;
Amati B.B., Goldschmidt-Clermont M., Wallace C.J.A., Rochaix J.-D.;
"CDNA and deduced amino acid sequences of cytochrome c from chlamydomonas reinhardtii: unexpected functional and phylogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                      Length 826;
                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                     92479 MW; 6A8898F7DF947389 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: Binds one heme group per molecule. SIMMILARITY: Belongs to the cytochrome c family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Mitochondrial matrix.
                                                                                                                                                                                                                                      70.0%; Score 35; DB 1; 1
66.7%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                            111 AA
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PIR; S29514; S29514.
HSSP; PO0055; LCR.
INTERPIC; IPRO00345; CytC_heme_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                            P15451;
01-APR-1990 (Rel. 14, Created)
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       441
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668
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888
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                                                                                                                                                                                                          826 AA;
                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                           52 RKTGSGFSY 60
                                                                                                                                                                                                                                                                                                         1 RGTGTGFAY 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytochrome c.
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Gaps

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STRAIN-White leghorn; TISSUE-Intestinal epithelium;
Xu J., Norman A.W., Henry H.L., de Boland A.R., Zanello L.P.;
Yu J., Norman A.W., Henry H.L., de Boland A.R., Zanello L.P.;
Yu J., Norman A.W., Henry H.L., de Boland A.R., Zanello L.P.;
Yu J., Norman A.W., Henry H.L., de Boland A.R., Zanello L.P.;
Yu J., Norman A.W., Henry H.L., de Boland A.R., Zanello L.P.;

RT intestinal epithelia cells.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: THE ISOROMA ALPHA-1S GIVES RISE TO L-TYPE CALCIUM
CURRENTS. LONG-LASTING (L-TYPE) CALCIUM CHANNELS BELONG TO THE
DIMUDROPRIDIDINES (DHP). PHENVILARIAKILAMNINES, BELONG TO THE
BY OMEGA-AGATOXIN-IIIA (OMEGA-AGA-IIIA). THEY ARE HOWEVER BY
COUPLING IN SKELETAL WINGCA-AGA-IIIA). THEY ARE HOWEVER BY
AGATOXIN-IVA (OMEGA-AGA-IVA). CALCIUM CHANNELS CONTRAINING THE
ACHDA-IS SUBBNIT PLAY AN INDERPRAYAN FOLE IN EXCITATION CONTRACTION
COUPLING IN SKELETAL WINGCA-AGA-IITA). THEY ARE MULTISUBUNIT
COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
COUPLING IN SKELETAL WINGCA-ENSITY SECONTATION
COMPLIES ACTIVITY. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1, ALPHA-1, SUBUNITS
CHANNEL ACTIVITY. THE AUXILLARY SUBUNITS BETA AND ALPHA-2/DELTA
ADDITIONAL GAMMA SUBUNIT IS PRESENT ONLY IN SKELETAL MUSCLE L-TYPE
CHANNEL ACTIVITY. THE AUXILLARY SUBUNITS BETA AND ALPHA-2/DELTA
ADDITIONAL GAMMA SUBUNIT IS PRESENT ONLY IN SKELETAL MUSCLE L-TYPE
CHANNEL BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY: AN
ADDITIONAL GAMMA SUBUNIT IS PRESENT ONLY IN SKELETAL MUSCLE L-TYPE
C-1- DOMAIN: EACH OF THE FOUR INFREMENCE SEGNENT (S4). S4 SEGMENTS
C-1- DOMAIN: THE LOOP BETWERN SEGMENT (S4). S4 SEGMENTS
C-1- DOMAIN: THE LOOP BETWERN SEGMENT SIN DOMAIN: THE LOOP BETWERN SEGMENT SIN DOMAIN: THE LOOP BETWERN SEGNES IN DOMES THE PROPERTY TON DOMAIN: THE BODD BETWERN SEGNES IN DOMES TO POSITIVELY CHARGED PROPERTY OF POSITI
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15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Voltage-dependent L-type calcium channel alpha-1S subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                             281 AA
                                                                                                                                                                                             PRT;
                                                                                                                                                                                          STANDARD;
                                                     RGTGFGFGH 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
1 RGTGTGFAY 9
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PTM: PHOSPHORYLATION BY CAPK STIMULATES THE CALCIUM CHANNEL FUNCTION (BY SIMILARITY). (BY SIMILARITY)

SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

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InterPro; IPR001682; Ca/Na_pore.
InterPro; IPR002077; Ca_channel.
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR000636; M+channel_nlg.
                                                                                                                     EMBL; AF007877; AAB63206.1; -
                                                                                                                                                          Pfam; PF00520; ion_trans; 1
38888888888888888888
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SZ OF REPEAT IV (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SX OF REPEAT IV (POTENTIAL).
SX OF REPEAT IV (POTENTIAL).
SX OF REPEAT IV (POTENTIAL).
SY OF REPEAT IV (POTENTIAL).
TO DIHYDROPYRIDINES (BY SIMILARITY).
CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
          Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
Calcium channel; Glycoprotein; Repeat; Multigene family;
Calcium-binding; Phosphorylation.
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S6 OF REPEAT III (POTENTIAL)
                                                                                                 CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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PRINTS; PR00167; CACHANNEL.
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Search completed: February 14, 2003, 11:16:21 Job time : 5.64516 secs

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February 14, 2003, 11:10:17 ; Search time 18.7258 Seconds (without alignments) 99.030 Million cell updates/sec
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GenCore version 5.1.3 . Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                   OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_bacteriap:*
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

	Description	08xt81 ralstonia s	083342 mirid herne	041940 mirid herne	OBrnt4 pseudomonas	09i4a8 pseudomonas	042245 brachydanio	O8vvu9 anabaena sp	093130 streptomyce	041689 vigna radia	Ogztra hordenm vnl	041601 triticum tu	040651 orvza sativ				
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	DB	16	12	12	7	16	13	16	16	10	10	10	10	16	10	17	16
	Query Match Length DB	416	644	644	685	685	266	502	519	101	146	150	165	198	360	401	423
æ	Query	82.0	78.0	78.0	78.0	78.0	74.0	74.0	74.0	72.0	72.0	72.0	72.0	72.0	72.0	72.0	72.0
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		060398 homo sapien Q8v1y0 treponema s Q65525 bovine grou Q82039 human rotav	099340 human rotav 099229 human rotav 0899b0 human rotav 01311 homo sapien 090188 homo sapien	Q99q95 homo sapien Q84cn0 methanosarc Q92g78 chlamydia t Q9pel0 xylella fas Q9en0 xylella fas Q94kf5 arabidopsis Q94515 arabidopsis Q8uvc7 agkistrodon
5 10 16 16	16 16 16	4 2 2 2 2	11111445	789 4 Q9BQC5 2115 17 Q9TQNO 41 2 Q9ZG78 99 16 Q9PE10 110 2 Q9AQM8 134 10 Q9FKF5 149 13 Q8UVC7
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ALIGNMENTS

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"Murine gammaherpesvirus-68 encodes homologues of thymidine kinase and glycoprotein H: sequence, expression, and characterization of pyrimidine kinase activity."; Virology 219:475-479(1996).
                                                                                                                                                                Milligan S., Efstathiou S., Stewart J.P., Nash A.A., Davison A.J.;
"Genetic content of murine gammaherpesviruses.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, U97553; AAB66394.1; -.
EMBL, AF105037; AAF19286.1; -.
Interprop. IPR001899; TK_herpes.
Pronom; PD001519; TK_herpes; 1.
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Pseudomonas.
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STRAIN=42A2 NCBI 40045;
Vidal-Mas J., Besumbes O., Manresa M., Busquets M.;
Vidal-Mas J., Besumbes O., Manresa M., Busquets M.;
Wilching, sequence and expression of a lipoxygenase gene of Pseudomonas aeruginosa 42A2 NCBI 40045.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF479686; AAL85880.1: -- DA863B58A47C4C29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 78.0%; Score 39; DB 2; Length 685; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                78.0%; Score 39; DB 12; Length 64
77.8%; Pred. No. 1.1e+02;
Live 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Linoleate oxygen oxidoreductase.
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01-MAR-2001 (TrEMBLrel. 16, Last seqt
01-MAR-2001 (TrEMBLrel. 16, Last seqt
01-JUN-2002 (TrEMBLrel. 21, Last anno
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Best Local Similarity 77.8
Matches 7; Conservative
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PA1169.
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"Murine gammaherpesvirus-68 encodes homologues of thymidine kinase and glycoprotein H: sequence, expression, and characterization of pyrimidine kinase activity.";
Virology 219:475-479(1996).
EMBL, X93468; CAA63755.1;
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STRAIN=WUMS, AND G2.4;
MEDLINE=97366649; Pubmed=9223479;
Virgin H.W. IV, Latreille P., Wamsley P., Hallsworth K., Weck K.E.,
Dal Canto A.J., Speck S.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete sequence and genomic analysis of murine gammaherpesvirus
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=WUMS;
Latraille P., Wamsley P., Waterston R.H.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 644 AA; 72256 MW; FDF782746EB557A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae.
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MEDLINE=96213518; PubMed=8638414;
Pepper S.D., Stewart J.P., Arrand J.R., Mackett M.;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NDC-2001 (TrEMBLrel. 19, Last annotation update)
Thymidine kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96213518; PubMed=8638414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001889; TK_herpes. Pfam; PF00693; TK_herpes; 1. ProDom; PD001519; TK_herpes; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virol. 71:5894-5904(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 78.0
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                     murid herpesvirus 4.
                                                                                                                                                                                                                                                                                                                                                  Gammaherpesvirinae.
NCBI_TaxID=33708;
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                 350 RGTGVGFCY 358
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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GAMMAHV ORF21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=33708;
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041940
ID 0419.
AC 0419.
DT 01-J
DT 01-J
DT 01-J
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08334
10 08334
2 08334
2 08334
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DT 01-N
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Anabaena sp. (strain PCC 7120).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1902;
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Hibi M., Hirano T.;
        STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E., W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                    Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
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                                                                                                                                                                                                                           Score 39; DB 16; Length 685; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF024536; AAB82272.1; -...
ZFIN; ZDB-GENE-990415-17; atch1.
InterPro; IFR001092; HLH_basic.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
SEQUENCE 266 AA; 28786 MW; 56A92494B52FEFB8 CRC64;
                                                                                                                                                                                                      685 AA; 74803 MW; B6A307595AE16A5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNV-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein All1875.
                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                   78.0%; Scot.
100.0%; Pred. No. 1.-
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                                                                                                                                   EMBL; AE004547; AAG04558.1; -.
HSSP; P08170; 2SBL.
InterPro; IPR000907; Lipoxygenase.
Pfam; PF00305; lipoxygenase;
PRINTS; PR00087; LIPOXYGENASE.
                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Loc 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                             opportunistic pathogen."
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                                                                                                                        Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                             Atonal homologue-1.
ATOH1 OR ZATH-1.
                                                                                                                                                                                           Complete proteome. SEQUENCE 685 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyprinidae; Danio.
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Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                               305 TGTGFAY 311
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Rabbinowitsch E., Salunders D., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                   Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
A Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
A Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous nitrogen-fixing
T. "Complete genomic sequence of the filamentous nitrogen-fixing
T. Cyanobacterium Anabaena sp. strain PCC 7120.";
I DNA Res. 81205-213(2001).
I EMBL: AP003587; BAR73574.1; --
R InterPro: IPR004843; M-Ppestrase.
R InterPro: IPR004844; S/T_phosphtse.
R FinerPro: IPR0149; Metallophos; 1.
R Fam: PF00149; Metallophos; 1.
W Hypothetical Protein; Complete proteome.
SEQUENCE 502 AA; 57518 MW; ASF008CBC2C59E61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 16; Length 502;
Pred. No. 1.8e+02;
1; Mismatches 1; Indels
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Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collins M., Harris D.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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                                                                                                    SEQUENCE FROM N.A.
MEDLINE=21595285; Pubmed=11759840;
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MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.08;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 77.07
Tr. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Putative protease.
SC03977 OR SCBAC25E3.14.
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                                 NCBI_TaxID=103690;
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                                                                                                                                                                                                          Gaps
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                            Vigna radiata.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Mature 417:141-147(2002).

EMBL; AL596551; CAC44701.1; -.

InterPro; IPR001254; Ser_protease_Try.

InterPro; IPR001254; Ser_protease_Try.

Pfam; PF00089; trypsin; 1.

Hydrolase; Protease; Serine protease.

SEQUENCE 519 AA; 50327 MW; 5CBBD5F0CC19E428 CRC64;
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                                                                                                                                                                      74.0%; Score 37; DB 16; Length 519; 75.0%; Pred. No. 1.9e+02; rive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-JUMBO; TISSUE-COTYLEDONS;
Lee K., Tan-Wilson A.L., Wilson K.A.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, 149382, AAA92062.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 101
101 AA; 11467 MW; 40E371DBB2D53818 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Carboxypeptidase II (Fragment).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                       101 AA.
                                                                                                                                                                                                       1; Mismatches
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InterPro; IPR000379; Ser_estrs_site.
Pfam; PF00450; Serine_carbpept; 1.
PRINTS; PR00724; CRBOXYPTASEC.
ProDom; PD001189; Serine_carbpept; 1.
PROSITE; PS00131; CARBOXYPEPT_SER_SER; 1.
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Q9ZTR3;
01-MAY-1999 (TrEMBLrel. 10, Created)
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01-NOV-1996 (TrEMBLrel. 01, Created)
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                                                                                                                                                                                                        6; Conservative
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228 GTGTGFVF 235
                                                                                                                                                                                                                                  2 GTGTGFAY 9
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NON_TER
SEQUENCE
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STRAIN-SILIANA; TISSUE=DEHYDRATED ROOT;
Labhilli M., Joudrier PH., Gautier M.F.;
Labhilli M., Joudrier PH., Gautier M.F.;
"Characterization of cDNAs encoding Triticum durum dehydrins and their expressions patterns in cultivars that differ in drought tolerance.";
Plant Sci. 112:219-230 (1995).
EMBL; X78431; CRA55194.1; -.
InterPro; IPR000167; Dehydrin; 1.
Pfam; PF00257; dehydrin; 1.
PROSITE; PS00013; DEHYDRIN_L; 1.
PROSITE; PS000823; DEHYDRIN_L; 2.
SEQUENCE 150 AA; 15163 MW; 3F3C846F526E03F8 CRC64;
                                  SEQUENCE FROM N.A.
STRAIN=CV. DICKTOO;
Choi D.-W., Zhu B., Close T.J.;
"The barley (Hordeum vulgare L.) dehydrin multigene family: sequences, chromosome assignments, and expression characteristics of 11 dhn genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.
                                                                                                                                                                                                                 STRAIN-CV. MOREX;
Choi D.-W., Close T.J.;
"Morex barley (Hordeum vulgare L. cv. Morex) dehydrin multigene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                             family.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                       of cv. Dicktoo.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                EMBL; AF043094; AADÓ2260.1; -.
EMBL; AF1841459; AAF01697.1; -.
InterPro; IRR001057; Dehydrin.
PROSITE; PS00315; DEHYDRIN_1, 1.
PROSITE; PS00315; DEHYDRIN_2; 2.
SEQUENCE 146 AA, 15128 MW; B979904F6800E299 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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87.5%;
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Best Local Similarity 87.57
Esc. 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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NCBI_TaxID=4513;
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Q40651
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Hagnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer. VCBI_TaxID=3827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Pfam; PF00083; sugar_tr; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 AA
                                                                                                                                                                             Interpro; IPR001563; Serine_carbpept.
Pfam; PF00450; serine_carbpept; 1.
PRINTS; PR00724; CRBOXPTASEC.
ProDom; PD001189; Serine_carbpept; 1.
PROSITE; PS001560; CARBOXYPEPT_SER_HIS; PROSITE; PS00131; CARBOXYPEPT_SER_HIS; Carboxypeptidase; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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Best Local Similarity
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                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                         29 TGTGFSY 35
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SEQUENCE
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                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
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MCEVOY S.M., Sheoran I.S., Saini H.S.;
"A rice cDNA encoding a late embryogenesis abundant protein.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; U60097; AAB03330.1;
EMBL; U60097; AAB0330.1;
Pfam: PPRO00157; dehydrin.
Pfam: PPRO0057; dehydrin: 1.
PROSITE; PSO00823; DEHYDRIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
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Pred. No. 1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   72.0%; Score 36; DB 10; Length 165; 87.5%; Pred. No. 83; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL, AP003193; BAB81873.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 198 AA; 21538 MW; E5E6F630D8434332 CRC64;
                                                                                                                                                                                                                                                         165 AA; 16671 MW; 581218E22BE37043 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-MRR-2002 (TrEMBLrel. 20, Last annotation update)
Serine carboxipeptidase (EC 3.4.16.6) (Fragment).
Cicer arietinum (Chickpea) (Garbanzo).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein CPE2167.
       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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85.7%;
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PubMed=11792842;
                                                              Oryza sativa (Rice)
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74 KGTGTGF 80
                                                                                                                    NCBI_TaxID=4530;
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Rawarabdayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Rawarabdayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
Oshima T., Kikuchi H.;
"Complete genome sequence of an aerobic thermoacidophilic
Crenarchaeon, Sulfolbus tokodaii strain?";
DNA Res. 8.123-140(2001).
EMBL; AP000987; BAB66918.1; -.
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STRAIN=CV. CASTELLANA; TISSUE=ETIOLATED EPICOTYLS;
Dopico B., Esteban R., Labrador E.;
Dopico B., Esteban R., Labrador E.;
A serine carboxipeptidase is expressed in chickpea epicotyls.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ271659; CAB71127.1;
HSSP; P08819; 1BCS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 72.0%; Score 36; DB 10; Length 36 Best Local Similarity 85.7%; Pred. No. 1.9e+02; Matches 6; Conservative 1; Mismatches 0; Indels
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SEQUENCE 401 AA; 43730 MW; 73BE08EA26463B17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 AA; 40153 MW; 140BEBACD0143FE0 CRC64;
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Search completed: February 14, 2003, 11:18:39 Job time : 20.8925 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein February 14, 2003, 11:04:17 ; Search time 40.6452 Seconds
(without alignments)
49.176 Million cell updates/sec Run on:

1 KASQSVDYDGDSYMN 15 US-09-701-001B-4 Perfect score: Sequence:

Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues rched: al number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

/SIDS2/gcgdata/geneseq/genesegp-embl/AA1990.DAT:*/SIDS2/gcgdata/geneseqp-embl/AA1991.DAT:*/SIDS2/gcgdata/geneseqp-embl/AA1992.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:* /SIDS2/gcgdata/geneseg/genesegp-embl/AA1995.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1996.DAT:* /SIDS2/gcgdata/geneseg/genesegp-emb1/AA2000.DAT:* /SIDS2/gcgdata/geneseg/genesegp-emb1/AA2002.DAT:* | SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb1,AA1981.DAT:*
| SIDS2/gcgdata/geneseqgeneseqp-emb1,AA1981.DAT:*
| SIDS2/gcgdata/geneseqg-emb2,AA1981.DAT:*
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| SIDS2/gcgdata/geneseqg-emb1,AA1981.DAT:*
| SIDS2/gcgdata/geneseqg-emb1,AA1981.DAT:*
| SIDS2/gcgdata/geneseqg-emb1,AA1986.DAT:*
| SIDS2/gcgdata/geneseqg-emeseqp-emb1,AA1986.DAT:*
| SIDS2/gcgdata/geneseqg-emeseqp-emb1,AA1986.DAT:*
| SIDS2/gcgdata/geneseqg-emeseqg-emb1,AA1988.DAT:*
| SIDS2/gcgdata/geneseqg-emeseqg-emb1,AA1988.DAT:*
| SIDS2/gcgdata/geneseqg-emeseqg-emb1,AA1988.DAT:*
| SIDS2/gcgdata/geneseqg-emeseqg-emb1,AA1988.DAT:* /SIDS2/gcgdata/qeneseq/geneseqp-embl/AA1997. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999. A_Geneseq_101002:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dР				
Result		Query				
No.	Score		Match Length DB	DB	ID	Description
		100 001	15	16.	AAP70195	MAN SEG LAST THE TANK
1	`	0.001	1	2	COTONIUS	שעה אור כוומד
2	79	100.0	12	19	AAW83027	Anti-Fas MAb HFE7A
٣	79	100.0	15	20	AAY23772	CDR of the light c
4	79	100.0	15	20	AAY18114	Light chain CDR fo
2	79	100.0	15	21	AAB14744	Mouse anti-Fas ant
9	79	100.0	15	21	AAW90894	Murine anti-Fas an
7	79	100.0	15	21	AAY59259	Antihody 4H5 L cha
80	79	100.0	15	21	AAY51136	Murine CD4/CD34 re
6	79	100.0	15	23	ABB74863	Humanised anti-Fas
10	79	100.0	15	23	ABB74909	Humanised anti-Fas

	11 12	79	100.0 100.0	19 103	15 21	AAR66143 AAY59263	tibod ly 4H5
	13			103	21	AAY51140 AAR33309	Murine derived pro
	15			106	21	AAY85197	Light chain amino
	17			111	14	AAR33305	MaE11 light chain.
	18 19		100.0 100.0	111	15	AAR55123 AAR55127	Mouse anti-HIV mu5 Mouse-human chimer
	20			111	15	AAR60302	Anti HIV antibody
	22			111	50	AAK6U3U6 AAY23781	Chimeric anti Hiv Light chain variab
	23			111	20	AAY18123 AAWO5650	Light chain sequen
	25			111	21	AAY85193	Light chain amino
	27			111	21	AAY5926/ AAY51144	Antibody 4H5 L cha Murine derived pro
	8 6			111	21	AAY51146	Murine derived pro
	30			111	13	AAB76939 AAR24575	Variable light cha
	31			113	22	AAB71895	Monoclonal antibod
	32			115	11	AAR04134	Anti-Leu 3a light
	34			131	10	AAR48618 AAP90543	Amino acids sequen
	35			131	11	AAR04132	Anti-Leu 3a light
	36 37			131	9 7	AAR75355	Humanized antibody
	38			131	50	AAY23779	chair
	39			131	20	AAY23771	Light chain variab
	4 1			131	707	AAY18126 AAY18118	chair
	42			132	16	AAR70189	MAb
	43			132	20	AAY23767	Light chain variab
	45			218	18	AAW13563	ised
						ALIGNMENTS	
RES	ILT 1						
AAR	AAR70195 TD AAR70195	U	է արժարժ.	1. Protein		ر در در د	
XX	CTO WITH	2				1	
A AC	AAR7019	5,					
DI.	20-SEP-	-1995	5 (first	st entry	γ)		
DE	MAb 3B9	Li	ght chain	in CDR.			
K K K K	Chimeric monoclona complemen	.0 ⊂ =	antibody; hu il antibody; itarity deter	~ Ɗ 0	ized ; in inq	humanized antibody; antibody en y; MAb; interleukin-4; IL-4; all. termining region.	engineering; allergy; CDR;
xx SO	Mus sp.						
XX	u u	5	_				
XX	2000		;				
PD	16-MAR-1	1995					
PF	07-SEP-	-1994	6	4WO-US10308	308.		
PR PR	07-SEP- 14-OCT-	-1993	55	3US-01173	366. 783.		
PA PA	(SMIK)		SMITHKLINE SMITHKLINE	VE BEECHAM VE BEECHAM	AM C	CORP. PLC.	
PI .	Gross M	MS,	Holmes	SD,	ylve	Sylvester DR;	
A D X	WPI; 19	995-1	123387/1	16.			
PT	Chimeric	c and	nd huma	humanised I	IL-4	monoclonal antibodies	(mAbs), derived

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                                                                      Spleen cells from mice immunized with human IL-4 were used to prepare hubridoms: which were screened for anti-IL-4 MAb secretion. Only
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                          hybridomas, which were screened for anti-IL-4 MAb secretion. Only clone 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were cloned into pGEM7f+ and transformed into E. coll bH5-alpha. A light chain cDNA clone was sequenced (AAQ83490) that encoded the protein given in AAR70189. 3 CDRS (AAR70195-97) were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                scleroderma; Goodpasture syndrome; Crohn's disease; sterility; heumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple solerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arterisocialerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy; complementarity determing region;
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from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions
                                                                                                                                                                                                                                           100.0%; Score 79; DB 16; Length 15; 100.0%; Pred. No. 1.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      monoclonal antibody; mouse; Fas; humanised antibody;
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apoptosis; autoimmune disease; Hashimoto's disease;
systemic lupus erythematosus; graft versus host disease;
Sjogren syndrome; pernicious anaemia; Addison's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kimihisa I;
                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-Fas MAb HFE7A light chain CDR-L1.
                                                Page 54; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hiroko Y, J
S, Shin Y,
                                                                                                                                                                                                                                                                                                                                                                                                                        AAW83027 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page 184; 292pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97JP-0276064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97JP-0082953.
97JP-0169088.
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                                                                                                                                                                                                                                                        Local Similarity 100.
Les 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hideyuki H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-543440/47.
                                                                                                                                                                                                            15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-1998;
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01-APR-1997;
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                                                                                                                                                                             identified
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW83027;
                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HFE7A;
                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
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This is the amino acid of complementarity determining region 1 (CDR-L1) of the light chain (see AAW83042) of murine anti-human Fas monoclonal antibody HFETA. The invention relates to antibodies, especially humanised antibodies (see AAW8304-29), recognising the Fas antigen. Such antibodies preferably comprise a heavy chain and light chains of HFETA. Humanised antibodies are produced by CDR grafting. The antibodies are capable of inducing apopticis in cornal cells. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune interactions, and also to treat such diseases, including autoimmune careful versus host disease, sjodren syndrome, pernicious anaemia, addisease, rheumatoid arthritis, autoimmune haemolytic anaemia, and disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Light chain variable region; interleukin-4; IL-4; antibody 389; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                         sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and
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                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 79; DB 19; Length 15; 100.0%; Pred. No. 1.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDR of the light chain variable region of antibody 3B9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          allergy; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  transplant rejection (all claimed).
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93US-0117366.
93US-0136783.
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KASQSVDYDGDSYMN 15
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                                                                                                                                                                                                                                                                                                                                                                                                       15 AA;
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14-OCT-1993;
07-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
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This sequence represents a light chain complementarity determining region (CDR) from an antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (19E) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody, interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma: anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease;
                                                                                                                                                                The present sequence represents a complementarity determining region (CDR) of the light chain variable region of murine interleukin-4 (IL-4) antibody 389. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reactions e.g. allergic thinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess endogenous IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans.
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                                                 Example 3; Column 43-44; 50pp; English.
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93US-0117366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 AA;
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st Local S
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conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14744-B14746 represent CDRs 1-3 of the light chain of the murine anti-human Fas monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                murine; complementarity determining region; CDR; human Fas;
Fas ligand; apoptosis modulator; programmed cell death;
autoimmune disease; allergy; attopy; arteriosclerosis; myocarditis;
cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
hepatitis; AIDS; graft rejection; light chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to compositions for the prevention or treatment
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100.0%; Pred. No. 1.6e-06;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                   Score 79; DB 20;
Pred. No. 1.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse anti-Fas antibody HFE7A light chain CDR1.
                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB14744 standard; peptide; 15 AA.
                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                      100.0%;
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Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                        versus host disease.
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This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

ligand system, by binding to Fas on the cells with an abnormal Fas/Fas

apoptosis in cells with a normal system, by inhibiting binding betwents

apoptosis in cells with a normal system, by inhibiting binding betwent

canti-memic, antidiabetic, anti-allergic, anti-arthritic, antiviral,

immunomodulatory, dermatological, immunosupressive, thyromimetic,

antirheumatic, nephrotropic, antiinfertility, neuroprotective,

antirheumatic, nephrotropic, antiinfertility, neuroprotective,

antirheriosclerotic, cardiant and hepatropic activity. (I) induce

apoptosis by binding to cell surface Fas or inhibit it by competitive

inhibition of ligand binding. (I) are used to treat and/or prevent

clupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft

versus host disease, Slorgen's syndrome, Goodpasture syndrome, Cohn's

disease, autoimmune hemolytic anemia, Sterility, myasthenia gravis,

cultiple sclerosis, Basedow's disease, thrombopenia purpura, insulin

dependent diabetes mellitus, allergy, arteriosclerosis, mycoarditis,

(B, C or D) or alcoholic), and transplant rejection. (I) selectively

cardiomyopathy the hours and

minibit apoptosis in normal cells but selectively induce it in abnormal
                                                                                                                                                                                                                                                                                                                                 Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia, Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cells. They bind to both human and murine Fas, so can be evaluated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tamaki I,
                                                                                                                                                                                                                                                                                            Murine anti-Fas antibody peptide fragment #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells with abnormal Fas-Fas ligand systems
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 98; 263pp; English.
                                                                                                                                                       AAW90894 standard; peptide; 15 AA.
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98JP-0276882
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                       1 KASQSVDYDGDSYMN 15
KASQSVDYDGDSYMN 15
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30-SEP-1998;
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murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a murine anti-Fas antibody peptide fragment described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. Sequences AAXF9259-61 represent the complementarity determining region (CDR)-1, CDR-2 and CDR-3 fragments in the L chain variable region of the antibody 4H5 respectively.
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                                                                                                                                                                                                                                                                                                                                         L chain variable region CDR1 fragment.
                                                                                                                                                                                                                                                                                                                                                                  CD4 antigen; anti-human; antibody; 4H5; drug; CDR; complementarity determining region.
                                                                                                          100.0%; Score 79; DB 21; 100.0%; Pred. No. 1.6e-06;
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                                                                                                                                   Mismatches
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Matches 15; Conservative
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                                                                               15 AA;
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                                                     of the invention.
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                                                                                 Sequence
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                                                                                                          Query Match
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AAY59259
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                                                  hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; complementarity determining region; CDR-1; light chain; murine.
                                             Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived complementarity determining region CDR-1 protein fragment which is used to illustrate the method of
                                                                                                                                                                                                                                                                                                                                                                                                              Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoletic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                light chain subunit; apoptosis; immunosuppressive; antiallergic; autoimmune disease; allergy; atopic.
             Murine CD4/CD34 recognizing antibody light chain CDR-1 region #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 79; DB 21; Length 15; 100.0%; Pred. No. 1.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised anti-Fas antibody related peptide SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                   Soka T, Morimoto I, Miyamura K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 76; 111pp; Japanese
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                                                                                                                                                                                                                                                                                                                   (ASAH ) ASAHI MEDICAL CO LTD
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                                                                                                                                                                                                                                                                    98JP-0163023
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                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-086720/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-APR-2002
                                                                                                                                                        WO9961629-A1
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                                                                                                                                                                                                                       24-MAY-1999;
                                                                                                                                                                                                                                                       25-MAY-1998;
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                                                                                                                                                                                       02-DEC-1999
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                                                                                                                            ds snw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a preventive or treating agent for diseases caused by abnormality in the Fas/Fas ligand system containing, as the active component, an antibody having a light chain subunit and a heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                       Drug containing humanised anti-Fas antibody, used for preventing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human: mouse; Fas/Fas ligand system; Fas; antibody; light chain; heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic; autoimmune disease; allergy; atopy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drug for preventing or treating e.g. autoimmune disease or allergy, comprises humanised anti-Fas antibody \,^{-}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised anti-Fas antibody related peptide SEQ ID NO 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                     Example 6 (Preparatory); Page 26; 194pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 79; DB 23; 100.0%; Pred. No. 1.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                        treating autoimmune diseases, allergy, and atopy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                            29-MAR-2000; 2000JP-0090918.
          28-MAR-2001; 2001JP-0093106
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                                                                            (SANY ) SANKYO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KASQSVDYDGDSYMN
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                                                                                                       WPI; 2002-145113/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                   15 AA;
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chain subunit and an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has antiallergic, immunosuppressive and apoptotic activity and is used for preventing and treating autolimmune diseases, allergy, atopy and others. The present sequence is that of a peptide useful to the
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR66140-R66146 are peptides complementary to the variable region of the CD-4 antibody, these peptides are fixed onto a claimed nonwoven fabric (average fibre dia. of 1-30 microns) coated with keto-alkyl halide functional groups. This material can be used as a filter for CD-4 positive cells in a medical treatment involving the extra-corporeal circulation of blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Material for collecting cells positive for CD-4 antibody - comprises nonwoven fabric having keto-alkyl halide functional gp
                                                                                                                  0;
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                                                                                              Length 15;
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                                                                                                                  Indels
                                                                                                                                                                                                                                                                                         CD-4 antibody variable region; complementary peptide; extra-corporeal blood circulation; cell filter material.
                                                                                                                                                                                                                                                                     CD-4 antibody variable region complementary peptide.
                                                                                            100.0%; Score 79; DB 23;
100.0%; Pred. No. 1.6e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY59263 standard; protein; 103 AA.
                                                                                                                                                                                                         AAR66143 standard; peptide; 19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 6; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                         93JP-0057206
                                                                                                                                                                                                                                                                                                                                                                                    93JP-0057206
                                                                                                                                                                                                                                                   (first entry)
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                               1 KASQSVDYDGDSYMN 15
                                                                                                                                   1 KASQSVDYDGDSYMN 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KASQSVDYDGDSYMN 15
                                                                                Query Match
Best Local Similarity
Local 15; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-346316/43.
                                                                                                                                                                                                                                                                                                                                                                                                                           (TOYM ) TOYOBO KK.
                                                                        Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 AA;
                                                                                                                                                                                                                                                                                                                                                                                   17-MAR-1993;
                                                                                                                                                                                                                                                                                                                                           JP06269663-A
                                                                                                                                                                                                                                                                                                                                                                                                         17-MAR-1993;
                                                                                                                                                                                                                                                  12-JUL-1995
                                                                                                                                                                                                                                                                                                                                                               27-SEP-1994
                                                     invention.
                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                               AAR66143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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AAY59263
                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                               AAR66143
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Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the L chain variable region of the antibody 4H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An antibody and the nucleic acid coding the antibody
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                                                                                       CD4 antigen; anti-human; antibody; 4H5; drug.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soka T, Morimoto I, Miyamura K;
                                              Antibody 4H5 L chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 15-16; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY51140 standard; Protein; 103 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                         (ASAH ) ASAHI KASEI KOGYO KK
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                                                                                                                                                                                                                                                                      98JP-0163034.
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17-APR-2000 (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ58662
                                                                                                                                                                              JP11332563-A
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                                                                                                                                                                                                                        07-DEC-1999.
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                                                                                                                                       Mus sp.
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This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
                               Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibodies capable of binding FCEL-bound IgE but which are substantially incapable of binding FCEH-bound IgE or inducing histamine release from mast cells or basophils, comprise a human Kabat CDR domain into which has been substituted a positionally analogous residue from a Rabat CDR domain of the murine anti-hulgE antibodies MAEII, MAEI3, MAEI5 or MAEI7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptide(s) binding to specific Fc epsilon receptors - act as IgE antagonists; useful for treating and preventing IgE-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 79; DB 21; Length 103; 100.0%; Pred. No. 1.4e-05; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody; high affinity; FCEH; low affinity; FCEL; IgE receptor; histamine; mast cell; basophil; Kabat; CDR; murine; MAE11; MAE13; MAE15; MAE17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR33309 standard; Protein; 106 AA.
                                                                                                          Claim 22; Page 79; 111pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders e.g. allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                             103 AA;
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N-PSDB; AAZ44204
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This sequence represents the light chain amino acid sequence of a mouse anti-human immunoglobulin E (IgE) antibody. The invention relates to a canti-human immunoglobulin E (IgE) antibody. The invention relates to a bispecific antibody that binds specifically to IgE when IgE is bound to its high affinity receptor (FCEH). The bispecific antibody comprises an IgE-binding arm with human framework residues of a recipient comprises an IgE-binding arm with human framework residues of a recipient residues, but with at least one human and replacing the analogous murine residue. The antibody also comprises an FV that is specific for a murine residue. The antibody also comprises an FV that is specific for a conformation of alternation of FCEL from cells (for research or therapy). The bispecific antibodies of the invention do not cause therapy). The bispecific antibodies of the invention do not cause therapy). The bispecific antibodies of the invention do not cause
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                                                                                                                                                                                                                                                                                                                                              Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FCEL; FCEH; low affinity binding receptor; high affinity binding receptor; allergy; diagnosis; treatment; histamine release; prevent; light chain.
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                           Length 106;
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                           100.0%; Score 79; DB 14;
100.0%; Pred. No. 1.4e-05;
Five. 0; Mismatches 0;
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94US-0185899.
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                                                                                               1 KASQSVDYDGDSYMN 15
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                                Query Match
Best Local Similarity
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1 KASQSVDYDGDSYMN 15

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Db 24 KASQSVDYDGDSYMN 38

Search completed: February 14, 2003, 11:15:44 Job time : 41.6452 secs Н

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Sequence 16, Appl
Sequence 16, Appl
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Sequence 6, Appli
Sequence 8, Appli
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32.575 Million cell updates/sec
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.: \cqn2_6/ptodata\f\/iaa/5B_COMB.pep:*
.: \cqn2_6/ptodata\f\/iaa\6B_COMB.pep:*
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.: \cqn2_6/ptodata\f\/iaa\Per\6B_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-483-632-58
US-08-579-378A-14
US-08-579-378A-18
US-08-483-636-2
US-08-483-636-2
US-08-483-632-2
US-08-887-352B-6
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US-08-466-151-6
US-08-466-151-6
US-08-401-845-8
US-08-491-845-16
US-08-491-845-16
US-08-491-845-16
US-08-491-845-16
US-08-491-82-73
US-08-483-636-73
US-08-887-352B-5
US-09-109-207C-5
US-09-109-207C-5
US-08-113-968-51
US-08-511-080-24
US-08-211-980-24
US-08-211-980-24
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US-08-211-980-24
US-08-211-980-24
US-08-211-980-24
US-08-211-980-24
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                                                                                                                                                                                       262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                  1 KASQSVDYDGDSYMN 15
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence 6, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 16, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 18, Appli		bisorders Le
111 4 US-09-109-207C-6 111 4 US-09-296-005-6 114 2 US-08-887-352B-10 114 4 US-09-296-005-10 218 2 US-08-887-352B-13 218 3 US-08-867-352B-13 218 4 US-09-109-207C-13 218 4 US-09-109-207C-13 218 4 US-09-109-207C-13 218 4 US-08-86-163B-9 41 3 US-08-86-163B-9 41 3 US-08-86-163B-9 114 2 US-08-53-477-5 114 4 US-09-296-005-9 114 4 US-09-296-005-9 115 4 US-08-887-352B-9 116 4 US-08-887-352B-9 117 2 US-08-887-352B-9 118 4 US-09-296-005-9 119 4 US-09-296-005-9	ALIGNMENTS	ion US/08483636 ion US/08483636 iii Stephen D. Mitchell S. ter, Daniel I S. ter, Daniel I I.4 Antibodiee: iii Treatment of IL4 Antibodiee: iii Forman Corp./Corporal Milline Beecham Corporal Mil
76 96.2 76 96.2 76 96.2 76 96.2 77 96.2 77 96.2 77 96.2 77 96.2 77 92.4 77 91.1 69 87.3 69 87.3 69 87.3		ULT 1 08-483-636-16 aquence 16, Application US/08 aquence 16, Application US/08 atent No. 591410 GENERAL INFORMATION: Stephen APPLICANT: Gross, Mitchell APPLICANT: Sylvester, Dani TITLE OF INVENTION: Recomb TITLE OF INVENTION: Treatm NUMBER OF SEQUENCES: 75 CORRESPENDENCE ADDRESS: ADDRESSEE: SmithKline Be ADDRESSEE: Intellectual STREET: P.O. Box 1539 / CITY: King of Prussia STATE: PA COUNTRY: USA STATE: PA COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: TBM PC COMPATION MEDIUM TYPE: Floppy disk COMPUTER: PA COMPUTER: TBM PC COMPATION MEDIUM TYPE: Floppy disk COMPUTER: PA COMPUTER: TBM PC COMPATION APPLICATION NUMBER: US/C FILING DATE: CLASSIFICATION DATA: APPLICATION NUMBER: US/C FILING DATE: 07-SPP-1999 RECISTRATION NUMBER: 9CT-1999 ATTORNEY/AGENT INFORMATION NAME: SULTON, Jeffrey A RECISTRATION NUMBER: 3CT-1999 ATTORNEY/AGENT INFORMATION TELECOMMUNICATION NUMBER: 3TELECOMMUNICATION NUMBER: 3TELECOMUNICATION NUMBER: 3TELECOMUNICATION NUMBER: 3TELECOMUNICATION NUMBER: 3TELECOMUNICATION NUMBER: 3TELECOMUNICATION NUMBER: 3
228 332 330 331 344 344 444 45 47 47 47 47 47 47 47 47 47 47 47 47 47		RESULT 1 US-08-483-636-16 Sequence 16, Appli Sequence 16, Appli Sequence 16 APPLICANT: GLAMATI APPLICANT: Syl TITLE OF INVENY SEQUENCE COUNTRY: US

Appli Appli Appli Appli

Sequence Sequence 6

14, 18, 22, 6,

Sequence Sequence

Sequence

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94080
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           US-08-466-151-6
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100.0%; Score 79; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                   Sequence 16, Application US/08483632
Patent No. 5928904
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 79; DB 2; Length 15; 100.0%; Pred. No. 2e-07; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 / UW2220 CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US CT/US/94/10308
FILING DATE: 07-SEP-1994
ATTONNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: 950186-3
TELECOMMUNICATION INFORMATION:
TELEPRONE: (215) 270-5024
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/483,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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; MOLECULE TYPE: protein
US-08-483-632-16
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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US-08-483-636-16
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100.0%; Pred. No. 1.9e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
Sequence 6, Application US/08466151
Patent No. 6037453
GANERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-ANG-1991
ATPGREVE APPLICATION NUMBER: 99.044
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAN: 560/525-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Fresta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/466,151
                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08466163B Patent No. 6329509
                                                                                                                                                                                           Genentech, Inc.
                                                                                                                                                                                                        STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 106 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.0
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: WinPati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
  0; Indels
                                                                                                                                                                                                                                                                                APPLICANT: EDA, Yasuyuki
APPLICANT: SHIOSAKI, Kouichi
APPLICANT: OSATOMI, Kiyoshi
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Browdy and Neimark
419 Seventh Street N.W. Ste. 300
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00039
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAEDA=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 73, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION:
                                                                                                                                                                             ; Sequence 16, Application US/08491845
; Patent No. 5773247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: MAE TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25,618
      ;
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INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                            MAEDA, Hiroaki
KIMACHI, Kazuhiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 111 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Browdy, Roger L. REGISTRATION NUMBER: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 KASQSVDYDGDSYMN 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KASQSVDYDGDSYMN 15
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        15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                     24 KASQSVDYDGDSYMN 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                           1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20004
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-483-636-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-491-845-16
                                                                                                                                                               US-08-491-845-16
                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                   APPLICANT:
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          Matches
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                                                                                                                                                                                                                                                                                        100.0%; Score 79; DB 4; Length 106; 100.0%; Pred. No. 1.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KIMACHI, KAZUHIKO
APPLICANT: SHIOSAKI, KIVACHI
APPLICANT: SHIOSAKI, KOUICHI
APPLICANT: OSATOMI, KIYOSAHI
APPLICANT: OSATOMI, KIYOSAHI
APPLICANT: TOSATOMI, KIYOSAHI
APPLICANT: TOSATOMI, KIYOSAHI
APPLICANT: OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 79; DB 1; 100.0%; Pred. No. 2e-06;
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419 Seventh Street N.W. Ste. 300
                                                                                                                                                                                                                                                                                                                                    Mismatches
              PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR PELING DATE: 1992-05-07
PRIOR PELING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00039
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/491,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: MAEDA=5
TELECOMMUNICATION:
TELEPHONE: (202) 628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-491-845-8; Sequence 8, Application US/08491845; Patent No. 5773247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 111 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Browdy, Roger L. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                            1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                        ) ORGANISM: Mus musculus
US-08-466-163B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-491-845-8
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                                                                                                                                                                               SEQ ID NO 6
                                                                                                                                                                                                                       TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
TITLE OF INVENTION: Treatment of 1L4 Mediated Disorders NUMBER OF SEQUENCES: 75
                                                                                                                                                                                           ZIP: 19406-0939
ZIP: 19406-0939
GOMPUTER READABLE FORM:
MEDIUM TYEP: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
                                                               ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 / UW2220 CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 75 CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corp./Corporate ADDRESSE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATPORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sutton, Jeffrey A. RECISTRATION NUMBER: 34,028 REFERENCE/DCKET NUMBER: P50186-3 TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 73, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (215) 270-5024
TELEPRAX: (215) 270-5024
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100.0
Matches 15, Conservative
                                          CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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                                                                                                                                                                             COUNTRY:
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GENERAL INCORNATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/11/366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY AGENT INFORMATION:
NAME: CATALOR
                                                                                                                                                                                                                                                                                                                                     PCT/US/94/10308
                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                P50186-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: U5/08/887,352B
FILING DATE: 03-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 5, Application US/08887352B
; Patent No. 5994511
                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P5C
TELECOMMUNICATION:
TELEPHONE: (215) 270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (215) 270-5024
TELEPAX: (215) 270-5020
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS
LENGTH: 111 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Genericch, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 KASQSVDYDGDSYMN 38
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GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypepti
FILE REFERENCE: P1123TI NG DATE: 1099-296,005
CURRENT APPLICATION NUMBER: US /08/887,352
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                            APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypept FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR PLING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 79; DB 4; Length 111; 100.0%; Pred. No. 2e-06; Live 0; Mismatches 0; Indels
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APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2CLD1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08466163B Patent No. 6329509
                                                                                                                                                      Sequence 5, Application US/09109207C Patent No. 6172213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 5, Application US/09296005; Patent No. 6290957
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                                  24 KASQSVDYDGDSYMN 38
         1 KASQSVDYDGDSYMN 15
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US-09-296-005-5
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 15; Conserve
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Best Local Similarity
Matches 15; Conserv
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US-09-296-005-5
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                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 111
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                                                                                                                                                                 100.0%; Score 79; DB 2; Length 111; 100.0%; Pred. No. 2e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GREERAL INFORMATION:
GREELCANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
APTILE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P0718P2C1D1
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAX-1992
PRIOR APPLICATION NUMBER: 07/744768
FILING DATE: 14-NG-1991
ATTORNEY/AGENT INFERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-7un-1995
APPLICATION NUMBER: 08/405617
                                                                                                                                                                                                                                                                                                                                                                                          08-466-151-2
quence 2, Application US/08466151
atent No. 6037453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P0
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                South San Francisco
California
                                                                                                                                                                                             100.0%;
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                                               111 amino acids
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Best Local Similarity
                                                                                    Amino Acid
                                                                                                           Linear
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                                                                                                        TOPOLOGY:
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                                    Query Match 100.0%; Score 79; DB 3; Length 115; Best Local Similarity 100.0%; Pred. No. 2e-06; Matches 15; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                      Sequence 24, Application 08/111080
Patent No. 5558865
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLE OF INVENTION: HIV Immunotherapeutics
TAPLE OF INVENTION: HIV Immunotherapeutics
CORRESPONDENCE: 38
CORRESPONDENCE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: 08/111,080
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100.0%; Pred. No. 2.1e-06;
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APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/748,562
FILING DATE: 22-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 310
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SOO ID NO: 24:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                     28 KASQSVDYDGDSYMN 42
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MOLECULE TYPE: protein
US-08-111-080-24
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US-08-111-080-24
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                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 51, Application US/08513968
Patent No. 6114143
GENERAL INFORMATION:
APPLICANT: EDA, Yasuyuki
APPLICANT: MAKIZUMI, Keiichi
APPLICANT: SHIOSAKI, Kouichi
APPLICANT: SHIOSAKI, Kouichi
APPLICANT: SHIOSAKI, Kazuhiko
APPLICANT: TOKIYOSHI, Kazuhiko
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,968 FILING DATE: 11-SEP-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR PLILING DATE: 1992-05-07
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 2
LENGTH: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 78913/1993
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 248633
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 25, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 KASQSVDYDGDSYMN 38
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                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Mus musculus
US-08-466-1638-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BROWDY
STREET: 419 Sevent
CITY: Washington
STATE: D.C.
COUNTRY: USA
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USA
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(without alignments)
44.001 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140259 seqs, 25548876 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                            US-09-701-001B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : peq:
                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                        Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

	Description	Sequence 16, Appl	9	Sequence 2, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 14, Appl	Sequence 58, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	6, A	Sequence 10, Appl	Sequence 9, Appli	Sequence 9, Appli	Sequence 13, Appl	Sequence 9, Appli	Sequence 8, Appli	Sequence 15, Appl
SUMMARIES	ID	US-09-879-461-16	US-09-802-096-6	US-09-802-077-2	US-09-802-096-2	US-09-920-171-5	US-09-879-461-14	US-09-879-461-58	US-09-879-461-2	US-09-917-410-2	US-09-903-327A-4	US-09-920-171-6	US-09-920-171-10	US-09-802-077-9	US-09-802-096-9	US-09-920-171-13	US-09-920-171-9	US-09-920-171-8	US-09-920-171-15
	DB	9 -	10	10	10	10	6	6	σ	10	6	10	10	10	10	10	10	10	10
	% Query Match Length DB	15	106	111	111	111	131	131	132	218	238	111	114	218	218	218	114	114	218
	% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	96.2	96.2	96.2	96.2	96.2	87.3	63.3	63.3
	Score	79	79	79	79	79	79	79	79	79	79	97	76	16	16	76	69	50	20
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10 US-09-920-171-17 10 US-09-920-171-19 10 US-09-920-171-24 10 US-09-920-171-22 11 US-09-920-171-23 12 US-09-920-171-23 13 US-09-920-171-23 14 US-09-920-171-7 12 US-10-027-770-2 15 US-09-920-171-7 15 US-09-920-171-7 16 US-09-920-171-7 17 US-09-171-7 18 US-09-171-7 19 US-09-174-886-89 19 US-09-174-886-89 10 US-09-174-886-85 10 US-09-173-111 10 US-09-173-111 10 US-09-773-111 10 US-09-773-111 10 US-09-773-111	10 US-09-840-459-54 10 US-09-840-459-58 9 US-09-968-851-38
218 2218 2218 2248 2269 2269 2211 2211 2221 2221 2221 2221	112 112 535
66 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	51.3 51.3 51.3
44 44 14 14 14 14 14 14 14 14 14 14 14 1	40.5 40.5 40.5
011020202020202020202020202020202020202	44 44 45

ALIGNMENTS

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Sequence 2, Application US/09802096
Patent No. US2010038839A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amen FILE REFERENCE: P0718P2C3US
CURRENT APPLICATION NUMBER: US/09/802,096
CURRENT FILING DATE: 2001-03-08
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APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION Method of Treating Allergic Disorders (as amended);
FILE REFERBNCE: P0718P2C2US
CURRENT APPLICATION NUMBER: US/09/802,077
CURRENT FILING DATE: 1999-01-03-08
PRIOR FILING DATE: 1999-03-15
PRIOR PLICATION NUMBER: US 08/405,617
PRIOR PLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR PLICATION NUMBER: US 07/894,495
PRIOR PLICATION NUMBER: US 07/89,495
PRIOR PLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
PRIOR FILING DATE: 1991-08-14
PRIOR FILING DATE: US 07/744,768
PRIOR FILING DATE: US 07/744,768
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                 Gaps
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PRIOR FILING DATE: 1995-03-15
PRIOR APLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-46
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
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3ER: US 08/405,617
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               1991-08-14
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ORGANISM: Mus musculus
          PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 6
LENGTH: 106
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Best Local Similarity
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                                                                                                            TYPE: PRT
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APPLICANT: Jardeus.
APPLICANT: Jardeus.
APPLICANT: Dardeus.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended CURRENT APPLICATION NUMBER: US/09/802,096
CURRENT FILING DATE: 1995-03-15
PRIOR PAPLICATION NUMBER: US 08/405,617
PRIOR PAPLICATION NUMBER: US 08/405,617
PRIOR PELING DATE: 1994-01-26
PRIOR FILING DATE: 1992-08-14
PRIOR PILING DATE: 1992-08-14
PRIOR PILING DATE: US 07/879,495
PRIOR PILING DATE: US 07/879,495
PRIOR FILING DATE: US 07/879,495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FREERL NO. USZULIUUS 2044AA.
FRIERAL INFORMATION.
FULLCANT: JAINGLEU, Paula M.
FPLICANT: JAINGLEU, Paula M.
FPLICANT: JAINGLEU, Paula M.
FREELICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
FILE REFERENCE: P0718P2C2US
CURRENT FILING DATE: 2001-03-08
FRIOR RILING DATE: 1995-03-15
FRIOR APPLICATION NUMBER: US 08/185,899
FRIOR FILING DATE: 1995-08-14
FRIOR FILING DATE: 1995-08-14
FRIOR FILING DATE: 1995-08-14
FRIOR FILING DATE: 1992-05-07
FRIOR PRICATION NUMBER: US 07/744,768
FRIOR FILING DATE: 1992-05-07
FRIOR PILING DATE: 1991-08-14
SEQ ID NO 6
FRIOR FILING DATE: 1991-08-14
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                                                                                                                                                                    100.0%; Score 79; DB 9; Length 15; 100.0%; Pred. No. 5.4e-07; tive 0; Mismatches 0; Indels
                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09802077
Patent No. US20010033842Al
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Patent No. US20010038839A1
LENGTH: 15 amino acids
                                                                                                                                                                                        Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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; ORGANISM: Mus musculus
US-09-802-077-6
                                                                                                                    US-09-879-461-16
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REFERENCE/DOCKET NUMBER: P50186-2
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APPLICANT: Jardieu, Paula M.
APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
FILE REFERENCE: P10.20203
CURRENT APPLICATION NUMBER: US/09/920.171
CURRENT APPLICATION NUMBER: US/09/920.171
PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR APPLICATION NUMBER: US 09/296,005
FROR PRILING DATE: 1997-07-02
FROR FILING DATE: 1999-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 - 709
Swedeland Rd.
CITY: King of Prussia
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Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant LL4 Antibodies Useful in
                                                                                                                                                                       100.0%; Score 79; DB 10; Length 111; 100.0%; Pred. No. 4.2e-06; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 79; DB 10; Length 111; 100.0%; Pred. No. 4.2e-06;
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US 07/744,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09920171 Patent No. US20020054878Al GENERAL INFORMATION:
                1991-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 19406-2799
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1991-06
NUMBER OF SEQ ID NOS: 64
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                                                                                                                ORGANISM: Mus musculus
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                                                                                                                                                                                                                15;
                                                                           LENGTH: 111
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09-920-171-5
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                                                           SEQ ID NO 2
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                                                                                                  TYPE: PRT
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ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UM2220 - 709
SWedeland Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treatment of IL4 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 79; DB 9; Length 131; 100.0%; Pred. No. 4.9e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: INP PC compatible
COMPUTER: INP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/879,461
FILING DATE: 12 Jun-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <unknown>
FILING DATE: <unknown>
APPLICATION NUMBER: US 08/136,783
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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APPLICATION NUMBER: 08/612,929
FILING DATE: <UNINCOMN-
FILING DATE: 14-0CT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; SEQUENCE DESCRIPTION: SEQ ID NO: 14: US-09-879-461-14
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                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 58, Application US/09879461 Publication No. US20020193575A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 131 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: King of Prussia
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Best Local Similarity 100.
Matches 15; Conservative
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Sequence 4, Application US/09903327A;
Patent No. US20020164333A1
; GENERAL INFORMATION:
APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Erguang;
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TAR
                                                                                                                                                                                                                                                                                                        MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR PREVENTION OF ACUTE ORGAN DAMAGE AFTER EXTRACORPOREAL BLOOD CIRCULATION
                                                                                                                                                                                                                                              APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
                                                                                                                                                                                                                                                                  CO, Man S. TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 79; DB 10; 100.0%; Pred. No. 8.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hanson, No. US20020098183Alman D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: CUNKOWN>
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII, WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/917,410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
TIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 26-Jul-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                            Sequence 2, Application US/09917410 Patent No. US20020098183A1 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
                          1 KASQSVDYDGDSYMN 15
                                                 1 KASOSVDYDGDSYMN 15
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Best Local Similarity
Matches 15; Conserv.
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US-09-903-327A-4
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Swedeland Rd.
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APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.

TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in Treatment of IL4 Mediated Disorders
                                                                                                                                                                                                                                                                  Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 79; DB 9; Length 132; 100.0%; Pred. No. 5e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                          Indels
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ADDRESSEE: SmithKline Beecham Corporation
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0
                                                                                                                                                                                                                                                           100.0%; Score 79; DB 9; 100.0%; Pred. No. 4.9e-06; tive 0; Mismatches 0;
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FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P50186-2
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APPLICATION NUMBER: US/09/879,461
                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 58: US-09-879-461-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 58:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 2:
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
                                                                                                           LENGTH: 131 amino acids TYPE: amino acid
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Publication No. US20020193575A1
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                                                                                     SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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ZIP: 19406-2799
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9-879-461-2
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GENERAL INFORMATION:
APPLICANT: Jardideu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amen
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TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
FILE REFERENCE: P0718P2C2US
CURRENT APPLICATION NUMBER: US/09/802,077
CURRENT FILING DATE: 2001-03-08
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-12
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: PCT/US92/06860
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
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                                                                                                                                                                                                                                                                                                                                                       Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: humanized maell, version 1, light chain US-09-802-077-9
                                                                                                                                                                                                                                                                                                                                   Score 76; DB 10; Length 11.
Pred. No. 1.3e-05;
Order 1.3e-05
                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Light chain sequence derived from MAE11 US-09-920-171-10
                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
FILE REFERENCE: P1123C2US
CURRENT APPLICATION NUMBER: US/09/920,171
CURRENT FILING DAFE: 2001-08-01
PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR FILING DATE: 1997-07-02
PRIOR PILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 10
LENGTH: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 07/744,768 PRIOR FILING DATE: 1991-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09802096 Patent No. US20010038839A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09802077 Patent No. US20010033842A1
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93.3%;
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APPLICANT: Jardieu, Paula M.;
APPLICANT: Presta, Leonard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 96.2
Best Local Similarity 93.3
Matches 14; Conservative
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Matches 14; Conserva
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OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody.
09-903-327A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6. Application US/09920171
; Batent No. US20020054878A1
; Patent No. US20020054878A1
; GENERAL INFORMATION:
   APPLICANT: Lowman, Henry B.
   APPLICANT: Jardieu, Paula M.
   APPLICANT: Lowe, John
   APPLICANT: Lowe, John
   APPLICANT: Lowe, John
   TILE REFERENCE: P1123C2US
   CURRENT APPLICATION INUMER: US/09/920,171
   CURRENT FILING DATE: 2001-08-01
   PRIOR FILING DATE: 1997-07-02
   PRIOR FILING DATE: 1997-04-21
   NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: F(ab) light chain sequence derived from MAE11 US-09-920-171-6
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Patent No. US20020054878A1
GENERAL INFORMATION:
APPLICANT: Lowman, Henry B.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 76; DB 10; Length 111; Pred. No. 1.3e-05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 79; DB 9; Length 238, 100.0%; Pred. No. 9.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
         TITLE OF INVENTION: GENE
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR ELING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               ery Match
                                                                                                                                                                                                                                                                                                                     NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-09-920-171-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O ID NO 6
LENGTH: 111
                                                                                                                                                                                                                                238
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                                                                                                                                                                                                            SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial sequence
FRATURE:
COTHER INFORMATION: humanized maell, version 1, light chain
US-09-802-096-9
CURRENT APPLICATION NUMBER: US/09/802,096
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 1050-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-86
PRIOR FILING DATE: 1994-01-86
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-17
PRIOR PILING DATE: 1992-05-07
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 9
LENGTH: 218
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: February 14, 2003, 11:21:31 Job time: 8.70968 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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using sw model - protein search, OM protein February 14, 2003, 11:12:02 ; Search time 15 Seconds
(without alignments)
96.134 Million cell updates/sec Run on:

US-09-701-001B-4 79

1 KASQSVDYDGDSYMN 15 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283224 seqs, 96134422 residues ched:

283224 tal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* Database

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Iq kappa chain V r		Ig kappa chain V r		chain V	chain V		chain	chain pr	chain V-	chain	chain V	Ig kappa chain V r	cal pr	chain	chain		light chain	>	kappa chain V-	kappa	kappa chain	tegrase/recom	kappa chain V	kappa chain V	g kappa chain '	chain V	g kappa chain	kappa chain V-
SUMMARIES	ID	S42193	A38601	KVMS43	KVMS83	KVMS08	KVMS69	KVMS10	S19971	PH1226	996608	KVMSC1	S19976	S19972	AI0948	B49442	PH0093	T03793	PH1079	KVMS80	696608	263596	S06732	A83958	S25462	S26343	S26344	KVMS54	VMS	S09963
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	% Query Match Length	81	93	111	111	111	111	110	112	131	111	111	112	112	282	96	109	551	102	111	111	115	120	303	91	107	107	108	111	111
	& Query Match	0	100.0	100.0	100.0	100.0	100.0	96.2	96.2	96.2	92.4	86.1	82.3	64.6	8.09	58.2	57.0	54.4	53.2	53.2	53.2	m	53.2	ന	77	51.9	$\overline{}$	51.9	$\overline{}$	_
	Score	79	79	79	79	79	79	16	16	16	73	68	65	51	48	46	45	43	42	42	42	42	42	42	41	41	41	41	41	41
	Result No.		7	e	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Ig kappa chain pre membrane-bound lyt	Ig kappa chain V r	Ig kappa chain V r	IG Kappa Chain V I	Ig kappa chain pre	Ig kappa chain V r	conserved hypothet	vacuolar sorting p	hypothetical prote	hypothetical prote	kinesin-related pr	hypothetical prote	Ig kappa chain V r	Iq kappa chain V r
KVMSM6 E83146	\$42186	A33730	A36259	C32513	S37202	A69012	T43335	H84590	H85633	A44259	T14513	S34095	B25155
7 7	a	2	7 (4 C	~	Н	~	7	7	-	7	~	2
131	91	101	112	132	111	154	176	406	869	716	808	83	8
51.9	51.3	51.3	51.3	51.3	50.6	50.6	50.6	50.6	50.6	50.6	50.6	50.0	50.0
													39.5 50.0

ALIGNMENTS

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Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: O'O-Ot-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C;Accession: 542193
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Ebr. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with s A;Reference number: 542193
A;Accession: 542193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:225456; NID:g407846; PIDN:CAA80943.1; PID:g407847 A;Note: the authors translated the codon GTT for residue 36 as Ala C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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Best Local Similarity 100.6
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-81 <MOJ>
                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
RESULT 1
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6 KASQSVDYDGDSYMN 20 g

RESULT 2

In Yappa chain V region (1G3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C;Accession: A38601
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
T; Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same anti
A;Reference number: A38601; MUID:91115823; PMID:1703527

A; Accession: A38601 A; Status: preliminary

A; Molecule type: mRN4 A; Residues: 1-93 <GOS> A; Cross-references: GB: M57978; NID:g196402; PIDN:AAA63359.1; PID:g196403 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin

Gaps ., 100.0%; Score 79; DB 2; Length 93; 100.0%; Pred. No. 3.8e-06; ative 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 15; Conservative

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1 KASQSVDYDGDSYMN 15

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A. Molecule type: protein
C. Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into
C. Superfamily: immunoglobulin munnoglobulin homology
C. Keywords: heterotetramer; immunoglobulin homology < IMM>
F: 16-94/Domain: immunoglobulin homology < IMM>
F: 23-92/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Mus musculus (Norson) Induse
() Species: Mus musculus (Norson) Induse
() Species: Mus musculus (Norson) Induse
() Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
() Accession: C01937; A01937
() Muscure 276, 785-790, 1978
() Mature 276, 785-790
() Mature 276
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                                                                                                                                                                                                                                                                                                                                                        A; Title: Rearrangement of genetic information may produce immunoglobulin diversity. A; Reference number: A93204; MUID:79073152; PMID:103003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             produce immunoglobulin diversity.
Ig kappa chain V region (PC7183) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C;Accession: B01937
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain V region (PC7769) - mouse C; Species: Mus musculus (house mouse) C; C;Date: 30-Jun-1993 #text_change 21-Jan-2000 C; Accession: BO1937; A01937; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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ilarity 100.0%; Pred. No. 4.5e-06;
Conservative 0; Mismatches 0;
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Matches 15; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 10-99 cMOO>
A; Residues: 10-99 cMOO>
A; Residues: 10-99 cMOO>
A; Residues: 10-99 cMOO>
A; Cross references: EMBL:225454; NID:9407842; PIDN:CAA80941.1; PID:9407843
A; Note: V*Reppa-21E; anti-collagen
A; Note: V*Reppa-21E; anti-collagen
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa also in some cases, such as IgA and IgM, the subunits associate into la C; Reprorating: immunoglobulin immunoglobulin homology
C; Reprorads: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:16-94/Domain: immunoglobulin predicted
                                                                                                                                                                                                                                               Ig kappa chain V region (PC7043) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C;Oate: 01-Sep-1981 #sequence_revision 01.Sep-1981 #text_change 21-Jan-2000
C;Oate: 01-Sep-1981; $42194; $42199; $42189; $42189; $42191; $42192
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: V-kappa-21E; anti-collagen
A; Note: V-kappa-21E; anti-collagen
A; Note: V-kappa-21E; anti-collagen
A; Note: V-kappa-21E; anti-collagen
A; Accession: $42190
A; Molecule type: DNA
A; Residues: 13-99 < MOF>
A; Cross-references: EMBL: 222450; NID: 9407838; PIDN: CAA80937.1; PID: 9407839
A; Note: V-kappa-21E; anti-collagen
A; Residues: 15-99 < MOA>
A; Accession: $42188
A; Note: V-kappa-21E; anti-collagen
A; Arcession: $42188
A; Note: V-kappa-21E; anti-collagen
A; Note: V-kappa-21E; anti-collagen
A; Arcession: $42188
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A;Note: V-Kappa-21E; anti-collagen
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A; Molecule type: DNA
A; Rosidues: 10-99 < MOY>
A; Cross-references: EMBL: Z25452; NID: 9407840; PIDN: CAA80939.1; PID: 9407841
pte: V-kappa-21E; anti-collagen
Ccession: $42192
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A.Residues: 1.111 <MBID
MMC, J.A.: Bona, C.A.: Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
5 KASQSVDYDGDSYMN 19
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esidues: 10-99 <MOJ>
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A; Residues: 12-99 <MOW>
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Matches 15; Conserv
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Cispecies: Mus musculus (house mouse)
Cispecies: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 31-Mar-2000
Cispecies: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 31-Mar-2000
Cispecies: District Novel 1980 #sequence_revision 31-Mar-2000
Rimckean, D.J.; Bell, M.; Potter, M.
Rimckean, D.J.; Bell, M.; Potter, M.
A; Potter, Matl. Acad. Sci. U.S.A. 75, 313-3917, 1978
A; Title: Mechanisms of antibody diversity; multiple genes encode structurally related A; Reference number: A93822; MUID:79012520; PMID:99744
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A; Residues: 1-111 <MCKS
C; Comment: This chain was isolated from a myeloma protein.
C; Compent: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibo A;Reference number: S09955; MUID:90269328; PMID:2347362 A;Accession: S09966
                                                              in tagpa chain precursor V region (M-T310) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PH1226
R;Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; L. A;Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and A;Reference number: PH1224; MUID:93077041; PMID:1446824
                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:g260766
A;Note: this mouse sequence was hybridized and fused with a human constant region gen
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin proficed <SIG>
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-31/Product: Ig light chain V region #status predicted <MAM>
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C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C;Accession: S09966
E;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
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A; Cross-references: EMBL:X51854; NID:955397; PIDN:CAA36147.1; PID:9930231
C; Superfamily: immunoglobulin V region; immunoglobulin homology
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93.3%; Pred No. 1.7e-05;
"**ematches 0;
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llarity 93.3%; Pred. No. 4.6e-05;
Conservative 0; Mismatches 1;
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Matches 14; Conservative
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Matches 14; Conserv
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A;Molecule type: mRNA
A;Residues: 1-131 <WEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title: Rearrangement of genetic information may produce immunoglobulin diversity A; Reference number: A93204; MUID: 79073152; PMID: 103003
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C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain V region (PC7210) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C;Accession: D01937; A01937
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A, Accession: S19973
A, Accession: S19973
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Fesidues: 1-112 < WEW>
A, Cross-references: EMBL: X65092; NID: 952292; PIDN: CAA46220.1; PID: 952293
A, Experimental Source: M-T404
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin
F; 16-94/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-112 (WHEI>
A;Cross-references: EMBL;X65091; NID:q52288; PIDN:CAA46219.1; PID:g52289
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                                                                              100.0%; Score 79; DB 1; Length 111; 100.0%; Pred. No. 4.5e-06; tive 0; Mismatches 0; Indels
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A, Description: Structural characterization of CD4 mAb.
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93.3%; Pred. No. 1.5e-05;
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F;16-94/Domain: immunoglobulin homology <IMM>F;23-92/Disulfide bonds: #status predicted
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Best Local Similarity 100.'
Matches 15; Conservative
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Matches 14; Conserv
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Query Match 60.8 Best Local Similarity 60.0 Matches 9; Conservative
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263 EALEPDDYDGDIYMN 277
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                                                                                                                                                                                                                                                                                  A; Accession: A10948
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: STY3863
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hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer C;C;Keywords: heterotetramer F;16-94/Domain: immunoglobulin homology <IMM>F;16-94/Domain: immunoglobulin predicted
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                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain V region (M-T413) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Mus musculus (house mouse)
Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
Accession: S19972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNÅ
A;Residues: 1-112 <WEI>
A;Cross-references: EMBL:X65093; NID:g52298; PIDN:CAA46221.1; PID:g52299
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dissendent, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
Mitted to the EMBL Data Library, March 1992
A. Description: Structural characterization of CD4 mAb.
A. Reference number: S19963
A. Accession: S19972
A. Status: preliminary
A. Status: preliminary
A. Status: preliminary
A. Residues: 1-112 < WEI>
A. Residues: 1-112 < WEI>
C. Superfamily: immunoglobulin v region; immunoglobulin homology
C. Superfamily: immunoglobulin homology < IMM>
F: 16-94/Domain: immunoglobulin homology < IMM>
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                                                                                                                                         Score 68; DB 1; Length 111;
Pred. No. 0.00031;
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80.0%; Pred. No. 0.001;
Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             ccession: 319976 "3544cmc_revision to replicate considerate considerate to the EMBL Data Library, March 1992 A; Reference number: S19963
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86.7%;
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66.78;
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Best Local Similarity 80.0°
Matches 12; Conservative
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Matches 10; Conservative
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:|||||||: |||: 24 RASQSVDYNAISYMH 38

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RESULT 14

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hypothetical protein STY3863 [imported] - Salmonella enterica subsp. enterica serovar C.Species: Salmonella enterica subsp. enterica serovar Typhi A.Note: this species has also been called Salmonella typhi C.Bate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 F.Parklil, J.: Dougan, G.: James, K.D.: Thomson, N.R.: Pickard, D.: Wain, J.: Church th. T.: Connerton, P.: Gronin, A.: Davis, P.: Davies, R.M.: Dowd, L.: White, N.: Farr Nature 413, 848-852, 2001 A.: Rutherford, K.: Simmonds, M.: Skelton, J.: Stevens, A. Althers: Parry, C.: Quail, M.: Rutherford, K.: Simmonds, M.: Skelton, J.: Stevens, A. Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A. Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 1944 chain V region (50.1) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C; Accession: 849442
R; Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapie, L.M.
Proteins 14, 499-508, 1992
A; Title: Crystallization, sequence, and preliminary crystallographic data for an anti A; Reference number: A49442; MUID: 93066166; PMID: 1438187
A; Reference number: A49442
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-96 cSTU
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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6; Mismatches
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Job time : 16 secs
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 14, 2003, 11:05:27 ; Search time 7.74194 Seconds (without alignments) 80.360 Million cell updates/sec Run on:

Title: Perfect score:

US-09-701-001B-4 79 1 KASQSVDYDGDSYMN 15 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 112892 seqs, 41476328 residues ched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

uc	musculu						s musculu	xenopus lae					s musculu	s musculu	s musculu	haemophilus	⊏		no sapien	=	no sapien	bovine papi	paenibacill	mus musculu	rattus norv	schizosacch	glycine max	caenorhabdi	antirrhinum	lytechinus	
Description	P01665 mus	P01666 mus	P01667 mus	P01669 mus	P01668 mus	P01664 mus	P01656 mus		P01654 mus	P01655 mus	P01674 mus	P01660 mus	P01662 mus	P01663 mus	_	ω	_	Q9m7r0 olea	. 000139 homo	P28740 mus	0					-	_	96	\sim	22	
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ID GI	KV3M_MOUSE	KV3N_MOUSE	KV30_MOUSE	KV3Q_MOUSE	KV3P_MOUSE	KV3L_MOUSE	KV3C_MOUSE	KIF2_XENLA	KV3A_MOUSE	KV3B_MOUSE	KV3V_MOUSE	KV3H_MOUSE	KV3J MOUSE	KV3K_MOUSE	KV3I_MOUSE	CCMH_HAEIN	KV3G_MOUSE	ALL8_OLEEU	KIF2_HUMAN	KIF2_MOUSE	KV2F_HUMAN	VE2_BPV4	THI1_PANTH	PDA4_MOUSE	PDA4_RAT	LSM6_SCHPO	IBB3_SOYBN	YI31_CAEEL	DAG ANTMA	LPSB_LYTPI	
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% Query Match	100.0	100.0	100.0	100.0	96.2		57.0	54.4	53.2		51.9	51.9	51.9	51.9	51.9	51.9	50.6	50.6	50.6	50.6	50.0	49.4	49.4	49.4	49.4	48.7		48.1		48.1	
Score	79	79	79	79	16	89	45	43	42	42	41	41	41	41	41	41	40	40	40	40	39.5	m	39	39	39	38.5	m	38	38	38	
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P09485 lytechinus	Ogog unman babil	P34311 caenorhabdi	P21037 vaccinia vi	P17371 vaccinia vi	P34586 caenorhabdi	P35448 xenopus lae	P38735 saccharomyc	Q9y4y8 homo sapien	P01615 homo sapien	P55646 rhizobium s	P58093 vibrio chol
LPSA_LYTPI	VE2_HPV66	YKR5_CAEEL	VC02_VACCC	VC02_VACCV	YN52_CAEEL	TSP1_XENLA	YHD5_YEAST	LSM6_HUMAN	KV2B_HUMAN	Y4RM RHISN	YV6A_VIBCH
7	Н	Η,	-	_	П	-	Н	Н	Н	Н	Н
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48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	47.5	47.5	47.5	46.8
38	38	38	38	38	38	38	38	37.5	37.5	37.5	37
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

111 AA.	pdate) update)	Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus	SEQUENCE. MEDLINE-79073152; PubMed=103003; Weigert M., Garmaitan L., Loh E., Schilling J., Hood L.E.; Mesarrangement of genetic information may produce immunoglobulin diversity.":		FRAMEWORK 1. COMPLEMENTARITY-DETERMINING-1. FRAMEWORK 2. COMPLEMENTARITY-DETERMINING-2. FRAMEWORK 3. FRAMEWORK 4. BY SIMILARITY. 7A5FCB586C306D29 CRC64;	ore 79; DB 1; Length 111; ed. No. 1.1e-06; Mismatches 0; Indels 0; Gaps	111 AA. ppdate) n update)
.D; PRT; Created)	Last sequence update) Last annotation update) egion PC 7043.	ata; Craniata; cia; Sciurognat	103003; Loh E., Sch information	ė.		Sc Pr 0;	NB; PRT; 111 AA. Created) Last sequence update) Last annotation update) region PC 7183.
ec.	Rel. 01, Rel. 38, n V-III r	etazoa; Chordata; Cheria; Rodentia; 3090;	L1. SEQUENCE. MEDLINE-79073152; PubMed=103003; Weigert M., Gatmaitan L., Loh E. "Rearrangement of genetic inform diversity.":	Nature 276:785-790(1978). PIR; A01937; KVMS43. HSSP; P80362; LWTL. InterPro; IPR003006; Ig_MHC InterPro; IPR003596; Ig_V. Ffam; PF00047; Ig; 1. SMART; SMO0406; IGv; 1.	1 23 24 38 39 53 54 60 61 92 93 101 102 111 111 111 111 AA; 12002 MW	tch 15; Conservative 15; Conservative KASOSVDYDGDSYMN 15 	STANDAR (Rel. 01, (Rel. 01, (Rel. 38,
	21-JUL-1986 (15-JUL-1999 (IG kappa chai Mus musculus	Eukaryota; Metazoa; Bammalia; Eutheria; NCBI_TaxID=10090;	SEQUENCE. MEDLINE=7907 Weigert M., ' "Rearrangeme	Nature 276:785-790(1978 PIR; A01937; KVMS43. HSSP; P80362; JWTL. InterPro; IPR003006; Ig. InterPro; IPR003596; Ig. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. Immunoqlobulin V region	DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN SEQUEND SEQUENCE 1	Query Match Best Local Similarity Matches 15; Conser 1 KASQSVDYDGDSY 1	RESULT 2 KV3N_MOUSE STAND2 AC P01666; DT 21-JUL-1986 (Rel. 01, 01, 11, 11, 12, 13, 10, 11, 13, 10, 11, 13, 10, 11, 13, 10, 11, 13, 10, 11, 13, 10, 11, 13, 10, 11, 13, 10, 11, 13, 10, 11, 11, 11, 11, 11, 11, 11, 11, 11

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Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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111 AA;
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P01669;
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KV3Q_MOUSE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                    MEDLINE=79073152; PubMed=103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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                                                                                                                                                          FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                 100.0%; Score 79; DB 1; Length 111; 100.0%; Pred. No. 1.1e-06; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                              11952 MW; 2058BB50CE306D31 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                         KV3O_MOUSE STANDARD; PRT; 111 AA. P01667; 21-JUL-1986 (Rel. 01, Created) 1-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 19 kappa chain V-III region PC 6308.
                                                                                                                                                                                                                              BY SIMILARITY.
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BY SIMILARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=79073152; PubMed=103003;
                                                                        Nature 276:785-790(1978).
PIR: B01937; KYMS83.
HSSP; P01679; ZFBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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InterPro; IPR003596; Ig_V.
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PIR; C01937; KVMSO8.
HSSP; P80362; IWIL.
                                                                                                                          Pfam; PF00047; ig. SMART; SM00406; IGv; 1. Immunoglobulin V region. DOMAIN
                                                                                                                                                                                                                                                                                       Conservative
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                       1 KASQSVDYDGDSYMN 15
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                                                                                                                                                                                                                                                111 AA;
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nes 15; Conserv
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KV30_MOUSE
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=79073152; PubMed=103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; Rearrangement of genetic information may produce immunoglobulin
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100.0%; Score 79; DB 1; Length 111; 100.0%; Pred. No. 1.1e-06; Live 0; Mismatches 0; Indels
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COMPLEMENTARITY - DETERMINING - 3.
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                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 7769.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Kappa chain V-III region PC 7210.
                                                                                                                                                                                                                                                                            111 AA.
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BY SIMILARITY.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV: 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diversity.";
Nature 276:785-790(1978).
PIR; E01937; KVMS69.
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                 1 KASQSVDYDGDSYMN 15
                                                                                                                                            24 KASQSVDYDGDSYMN 38
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Walczak C.E., Mitchison T.J., Desai A.;
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                        KV3C_MOUSE
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              RESULT 7
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MCKean D.J., Bell M., Potter M.;
MCKean D.J., Bell M., Potter M.;
Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-i - MSCELLAMBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
PIR; A01936; KVMSCI.
HSSP; P80362; IMTL.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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COMPLEMENTARITY - DETERMINING - 1.
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                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region CBPC 101.
                                                                                                                                                                                                                                                                                            111 AA.
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                                                                            FRAMEWORK-1.
                                                                                                                  FRAMEWORK-3
                                                                                               FRAMEWORK-2
                                                                                                                                    FRAMEWORK - 4
       PIR; D01937; KVMS10.
HSSP; P01679; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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Interpro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMRAT; SM00406; IGv. 1.
Immunoglobulin V region.
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                                                                                                                                                                                                        Matches 14; Conservative
Nature 276:785-790(1978).
                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                 110 AA;
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NON_TER
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KV3L_MOUSE
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                 Gray W.R., Dreyer W.J., Hood L.E.;
"Mechanism of antibody synthesis: size differences between mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Kinesin-like protein KIF2 (Kinesin-related protein XKIF2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11904 MW; 4FE7ABC9DF0FC125 CRC64;
                                                                                                                                                                                                                                                                                                                                                         Science 155:465-467(1967).
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR: A01910; KVMS80.
                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P01679; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00396; Ig_V.
Pfam; PF00047; Ig; 1.
IMMRT; SM00406; IGv; 1.
Immunoglobulin V region; Bence-Jones protein.
                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region MOPC 70.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.66;
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111 AA
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  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96140638; PubMed=8548824;
                                                                                                                                                                                                                                                                                MEDLINE=67056897; PubMed=4162931;
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    STANDARD;
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24 RASESVDNSGISFMN 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                       kappa chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Walczak C.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIF2_XENLA
KV3C_MOUSE
P01656;
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SEQUENCE
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                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and restrictiutions as long as its content is in no way entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                     SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. MCAK/KIF2
"XKCM1: a Xenopus kinesin-related protein that regulates microtubule dynamics during mitotic spindle assembly.", Cell 84:37-47(1996).
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE PC 2880 AND PC 1229 SEQUENCES ARE IDENTICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                DROSITE: PSO0411; KINESIN_MOTOR_DOMAIN1; 1.

PROSITE: PSSO067; KINESIN_MOTOR_DOMAIN2; 1.

MOTOR protein; Microtubules; ATP-binding; Coiled coil.

DOMAIN 193 542 GLOBULAR (POTENTIAL).

DOMAIN 543 682 KINESIN-MOTOR (BY SIMILARITY).

NP_BIND 288 295 ATP (BY SIMILARITY).

SEQUENCE 682 AA; 77414 MW; 3DA295BB319063F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      54.4%; Score 43; DB 1; Length 682; 63.6%; Pred. No. 11;
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COMPLEMENTARITY - DETERMINING - 3.
                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-III region PC 2880/PC 1229.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAMEWORK - 2
                                                                                                                                                                                        HSSP; P1719; 3KAR.
InterPro; IPR001752; Kinesin_motor.
Pfam. PF00225; Kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
                                                                                                                                                                              EMBL; U36486; AAC59744.2; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=79073152; PubMed=103003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP, P80362; 1WTL.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003566; Ig_V.
Pfam: PF00047; ig; 1
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 63.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 276:785-790(1978)
-!- MISCELLANEOUS: THE P
PIR; A01930; KVMS80.
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625 TEEVDYDADSY 635
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                                                    SUBFAMILY.
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KV3A_MOUSE
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                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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                                   53.2%; Score 42; DB 1; Length 111; 60.0%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.2%; Score 42; DB 1; Length 112; 60.0%; Pred. No. 2.2;
                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
111 AA; 11980 MW; AFEAC6A9D26FC12D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5F0DD25EE20BE611 CRC64;
                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 7132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=79073152; PubMed=103003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
MEDLINE=79073152; PubMed=103003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 276;785-790(1978).
PIR, A01930; KWMS80.
HSSP, P01679; 2FBJ.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 1g; I.
SMART; SMO4406; IGY; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12054 MW;
                                                                       Conservative
                                                                                                                                                                                                                                  STANDARD;
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24 RASESVDNYGISFMN 38
                                                                                                      1 KASQSVDYDGDSYMN 15
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24 RASESVDNYGISFMN 38
                                                Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 AA;
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les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                              KV3B_MOUSE
P01655;
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P01674;
                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
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SEQUENCE
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111 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A01935; KVMSM6.
HSSP; P01679; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                  Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||:||| |:|:||
24 RASESVDSYGNSFMH 38
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                                                                                                                      1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                        24 RASESVDSYGNSFMH 38
                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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339
54
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111
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                                                                                                                                                                                                                                             KV3J_MOUSE
P01662;
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NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   related mouse kappa variable regions.";
Proc. Natl. Acad. Scl. U.S.A. 75:3913-3917(1978).
Proc. Natl. Acad. Scl. U.S.A. 75:3913-3917(1978).
PIR: A01934; KVMS37.
HSSP: P01679; ZPRJ.
InterPro: IPR003006; Ig_MC.
InterPro: IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE-79073152; PubMed=103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; Weigert M., Gatmaiten L., Information may produce immunoglobulin
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin diversity."; Nature 276:785-790(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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COMPLEMENTARITY - DETERMINING - 3.
                                                                                                                                                                                                                  COMPLEMENTARITY - DETERMINING-1.
                                                                                                                                                                                                                                                                           FARMENCEN - 3 .
COMPLEMENTARITY - DETERMINING - 3 .
                                                                                                                                                                                                                                                   COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 1; Length 108; Pred. No. 3.1; 4; Indels
                                                                                                                                                                                                                                                                                                                                                           D40921D18DAC4B9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1996 (Rel. 38, Last annotation update)
19 Kappa chain V-III region PC 3741/TEPC 111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAMEWORK-4.
BY SIMILARITY.
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                                                                                                                                                                                                   FRAMEWORK - 1
                                                                                                                                                                                                                                      FRAMEWORK-2
                                                                                                                                                                                                                                                                       FRAMEWORK - 3
                                                                                                                                                                                                                                                                                                           FRAMEWORK - 4
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                                                                    PIR; A01940; KYMS54.
HSSP; P80362; 1WTL.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                               11699 MW;
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60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 60.0
Matches 9; Conservative
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SMART; SM00406; IGv; 1.
Immunoglobulin V region
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                                                                                                                                                                                                                                                                                                                                                               108 AA;
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P01660;
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MCKean D.J., Bell M., Potter M.;
McKean D.J., Bell M., Potter M.;
Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diversity.";
ature 276.785-790(1978).
-i - MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE (PC 9245).

BEDLINE-79073152; PubMed-103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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COMPLEMENTARITY-DETERMINING-1.
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51.9%; Score 41; DB 1; Length 111; 53.3%; Pred. No. 3.2;
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region ABPC 22/PC 9245.
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McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Ig kappa chain V-III region PC 4050.
Mus musculus (Mouse).
Eukaryota: Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burstein Y., Schechter I., "Priminal extra peptide segments linked to the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes."; Biochemistry 17:2392-2400(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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MEDLINE=73140225; PubMed=4691517;

McKean D.J., Potter M., Hood L.E.;

"Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.";
                                                                                                                 Welgert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                                                                                                                                                                                                                                                                                               12005 MW; 39D87619313453CB CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region MOPC 63 precursor.
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                                                                                                  MEDLINE=79073152; PubMed=103003;
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MEDLINE=78235887; PubMed=98179;
                                                                                                                                           diversity.";
Nature 276;785-790(1978).
PIR; A01935; KVMSM6.
HSSP; P01679; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003566; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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P01661;
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                                                                                                                                                                                                                                                       2; Indels
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 Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
                                                                                                                                                                                      BY SIMILARITY.
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        PIR, A01935; KVMSM6.
HSSP; P01679; 2FBJ.
InterPro; IPR0033006; Ig_MHC.
Pfam; PP00047; 1g; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
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44 RASESVDSYGNSFMH 58
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Best Local Similarity
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February 14, 2003, 11:10:17; Search time 31.2097 Seconds (without alignments) 99.030 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                 671580 seqs, 206047115 residues
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Maximum DB seq length: 200000000
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79
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Sequence:
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Maximum Match 100% Listing first 45 summaries sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_human:*
sp_invertebrate:* sp_unclassified:*
sp_rvirus:* sp_vertebrate:* sp_bacteriap:* sp_organelle:* sp_phage:* sp_plant:*
sp_rodent:* sp_virus:* SPTREMBL_21:* sb_mhc:* Database :

Post-processing: Minimum Match 0%

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

	Description	Q8zku0 salmonella	Q8z2s9 salmonella	Q9njd9 onchocerca	Q9c107 schizosacch	P97596 rattus norv	Q9w210 drosophila	P93370 nicotiana t	Q9lvx3 arabidopsis	Q9aqy5 polytomella	Q925s1 mus musculu	Q9ka25 bacillus ha	Q9ji46 mus musculu	O95989 homo sapien	Q9x6v5 pseudomonas	Q9hx24 pseudomonas	Q9srp5 arabidopsis
SUMMARIES	ΠD	Q8ZKUO	082289	6GLN6C	29C107	P97596	O9W2L0	P93370	Q9LVX3	Q9AQY5	092551	Q9KA25	09JI46	095989	Q9X6V5	Q9HX24	Q9SRP5
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	% Query Match Length DB	282	282	542	815	137	186	551	1868	153	218	303	168	172	336	340	131
	% Query Match	60.8	8.09	55.7	55.7	54.4	54.4	54.4	54.4	53.2	53.2	53.2	51.9	51.9	51.9	51.9	50.6
	Score	48	48	44	44	43	43	43	43	42	42	42	41	41	41	41	40
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Q9SRP4 O27163 O42711 Q9D058 Q92L50	Q9WV63 Q86071 Q9SIV3	Q9H2V9 Q9D6X1 Q9G8KW9	Q8R4E1 O8TB96	Q9BRE2	054744 091W03	Q9SW62 Q9FH44	Q8QS29	Q9JL80	Q94MM9	Q05432			-		027482
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ALIGNMENTS

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STRAIN=LT2 / SGSC1412 / ATCC 700720;

STRAIN=LT2 / SGSC1412 / ATCC 700720;

MEDLINE=21534948; Pubbed=11677609;

McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

Leonard S., Nauyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                Bacteria; Próteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                               Nature 413:852-856(2001).

EMBL; AE008887; AAL22854.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 282 AA; 31896 MW; 192C4AE31679D2C6 CRC64;
                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putalive cytoplasmic protein.
                             282 AA.
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263 EALEPDDYDGDIYMN 277
                               PRELIMINARY;
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Best Local Similarity
Matches 9; Conservat
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NCBI_TaxID=602;
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380 QEIDSDGDGYIN 391
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                                                                                                                                                              STRAIN-CT18;
MEDLINE-21534947; PubMed-11677608;
MEDLINE-21534947; PubMed-11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20278137; PubMed=10816503;
Lizotte-Waniewski M., Tawe W., Guiliano D.B., Lu W., Liu J.,
Williams S.A., Lustigman S.;
"Identification of potential vaccine and drug target candidates by
expressed sequence tag analysis and immunoscreening of Onchocerca
Nolvulus larval cDNA libraries.";
Infect. Immun. 68:3491-3501(2000).
EMBL; AR153720; AAR64251.1;
InterPro; IPR002048; EF-hand.
Pfam; PP000365; Efhand; 10.
                                                                                                                                                                                                                                                                                         "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18."; Mature 413:848-8522(2001).

EMBL; AL627279; CAD06011.1; --
Hypothetical protein; Complete proteome.

SEQUENCE 282 AA; 31930 MW; EBCE0B08D96E877 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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PROSITE; PSO0018; EF_HAND; UNKNOWN_7.
SEQUENCE 542 AA; 61269 MW; 94E3D57FB72D805B CRC64;
                          01-MAR-2002 (TrEMBLrel. 20, Created)
U-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein STY3863.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
      282 AA
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2; Mismatches
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     PRT;
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    PRELIMINARY;
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Best Local Similarity 58.37
نام 7; Conservative
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263 EALEPDDYDGDIYMN 277
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Best Local Similarity
                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                        Salmonella typhi
                                                                                                                              NCBI_TaxID=601;
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             Q8ZZS9;
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Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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WEDLINE=97149430; PubMed=8996238;
MEDLINE=97149430; PubMed=8996238;
Lutzelschwab C., Pejler G., Aveskoph M., Hellman L.;
"Secretoxy granule proteases in rat mast cells. Cloning of 10
different serine proteases and a carboxypeptidase A from various rat
J. Exp. Med. 185:13-29(1997).
EMBL; U67913; AAB48266.1; -.
HESSP: PO44187; 2CP1.
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WOOD V., Rajandream M.A., Barrell B.G., Seeger K., Harris D.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
R EMBL; AL590065; CAC36919.1; -.
R InterPro; IPR001680; WD40.
R SMARK; SMO320; WD40; 6.
R PROSITE; PS50082; WD_REPEATS_2; 1.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
R Hypothetical protein; Repeat; WD repeat.
W Hypothetical protein; Repeat; WD repeat.
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                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 91.0 kDa protein.
SPAPBIE7.02C.
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Pfam; PF00089; trypsin; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
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PRELIMINARY;
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DNA Res. 7:131-135(2000).
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Bazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Berman B.P., Bhandrai D., Bolshkov S.,
RA Ballew R.M., Basu D.A., Butler B., Bhandrai D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dawis S.P.,
A Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Dunkov B.C.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleistchman W.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
Cabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,
RA Jalai M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,
A Jalai M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.
A Jalai M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.
A Merkulov G., Milshina N.V., Moberry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Moberry C., Morris J., Moshrefi A.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Sanith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Shier E., Spradling A.C., Stapleton M., Weissenbach J.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Weissenbach J.,
RA Shar R., Therefor C., Turner R., Weissenbach J.,
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                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                              Gaps
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                                                           Score 43; DB 11; Length 137; Pred. No. 10;
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137 137
137 AA: 15019 MW; 83632B52786085BF CRC64;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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InterPro; IPR002048; EF-hand.
                                                                  54.48;
53.38;
                                                                                                Conservative
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01-JUN-2002
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0T-2000 (TrEMBLrel. 20, Last annotation update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
Genomic DNA, chromosome 3, Pl clone: MGF10.
Arabidopsis thaliana (Mouse-ear Cress).
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dash S., Lu Y., Harrington H.M.; "Molecular cloning and characterization of a tobacco calmodulin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
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                                                                                                 54.4%; Score 43; DB 5; Length 186; 50.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana
NCBI_TaxID=4097;
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                                                                                                                                                      Indels
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U58971; AAB37246.1; -.
SEQUENCE 551 AA; 61598 MW; 813879E25125C374 CRC64;
                                                    186 AA; 21301 MW; 7B8A6AA5A87AFAFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                      5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicotiana tabacum (Common tobacco).
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Pfam; PF00036; efhand; 2.
ProDom; PD000012; EF-hand; 1.
SEQUENCE 186 AA; 21301 MW:
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Best Local Similarity
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les 7; Conserv
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                                                                                                              Query Match
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RESULT 10
                           092581
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                                         δλ
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J. Biol. Chem. 276:11302-11309(2001).
-!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. SUBUNIT 2 TRANSFERS THE ELECTRONS FROM CYTOCHROME C VIA ITS BINUCLEAR COPPER A CENTER TO THE BIMETALLIC CENTER OF THE CATALYTIC SUBUNIT 1 (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ÁCTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME C + 2 H(2)O.
-!- COFACTOR: COPPER A AND HEME GROUP (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INNER MEMBRANE (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 2 FAMILY.
EMBL, AF305542; AAK32116.1; -.
EMBL, AF305079; AAK30366.1; -.
HSSP; P18400; 1CXX.
                                                                                                                                                                                                                                                                                                                                                                                      Polytomella sp. 'Pringsheim 198.80'.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Polytomella.
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                                                                                                          54.4%; Score 43; DB 10; Length 1868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.2%; Score 42; DB 10; Length 153; 61.5%; Pred. No. 17;
                                                                                                                                           5; Indels
         InterPro; IPR001395; Aldo/ket_red.
InterPro; IPR000345; Cytc_heme_bind.
PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SEQUENCE 1868 AA; 206712 MW; 0799ADC38CCOC5F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PROILEG; CYCOXIDASEII.
ProDom; PD000131; Copper_CuA; 1.
PROSITE; PS00078; COX2; 1.
COPPer: Inner membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane.
SEQUENCE 153 AA: 17219 MW; A69030F3E4746238 CRC64.
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                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CYLCCHrome C oxidase polypeptide II (EC 1.9.3.1).
                                                                                                                       2e+02;
                                                                                                                                                                                                                                                                                   PRT; 153 AA.
                                                                                                                                         1; Mismatches
                                                                                                                            Pred. No.
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InterPro; IPR002429; Cyt_c_ox_2.
EMBL; AB018114; BAB02691.1; -.
                                                                                                                       60.08;
                                                                                                                                                                                       STRAIN-PRINGSHEIM 198.80; PubMed=11094061;
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                    1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00116; COX2; 1
                                                                                                                      Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=37502;
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                                                                                                         Query Match
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                                                                                                                                     Matches
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Cui D., Zeng G., Yan X., Li X., Su C.; "Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain.";
                                                                                                                                                                                                                                                                                                                                     "Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice."; World J. Gastroenterol. 6:709-717(2000).
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EMBL; APO01515; BAB06184.1; -. HSSP; P21891; 1A0P.

Interpro; IPR002104; Phage_integrase.

InterPro; IPR004107; Phage_integrase.

Pfam; PF00589; Phage_integrase; 1.

Pfam; PF00589; Phage_integrase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
EMBL; AF240168; AAK43733.1; -.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
NON_TER 218
SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;
                                                                                                                                                                                                                                                                                             Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.2%; Score 42; DB 11; Length 218; 60.0%; Pred. No. 25; 3; Indels
                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9KA25,
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||:||| | |:||
159 RASESVDNIGISFMN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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STRAIN=C-125 / JCM 9153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Integrase/recombinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus halodurans.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Best Local Similarity
                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                              PubMed=11819679;
                                                                                                     MRP5 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CODV OR BH2465
                                                                                                                                                                                                                                                          STRAIN=BALB/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Horikoshi K.;
Q925S1
Q925S1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9KA25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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; 0

Gaps

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3; Indels

2; Mismatches

8; Conservative

Matches

||| : |: |||| 36 ASQPIQYNFDSYM 48 2 ASQSVDYDGDSYM 14

0;

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Conservative
                                                                                                                                                                                                                                      Best Local Similarity 53.83
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa.
                                                                                                                                                          Pfam; PF00293; NUDIX;
                                                                                                                                                                                                                                                                           1 KASQSVDYDGDSY 13
                                                                                                                                                                                                                                                                                                  5 KSNOTRTYDGDGY 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 AVDFDGDGHIN 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 SVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=287;
                                                                            TISSUE=UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huletsky A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas
                                                                                                                                                                                              Hydrolase.
SEOUENCE
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                                                                                                                                                  InterPro;
                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9HX24;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DIPHOSPHOINOSITOL polyphosphate phosphohydrolase (NUDIX (Nucleoside diphosphate linked MOIETY X)-type motif 3).
                                                          Gaps
                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 21, Last annotation update)
Diphosphoinositol polyphosphate phosphohydrolase (Nudix (nucleotide diphosphate linked molety X)-type motif 3).
NUDT3 OR DIPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 53.8%; Score 41; DB 11; Length 168; Local Similarity 53.8%; Pred. No. 28; 7; Conservative 3; Mismattle
                                 Score 42; DB 16; Length 303;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                       Chu C., Timo K., Lisanti M., Burstein D., Kohtz D.; "Ectopic Expression of Diphosphoinositol Polyphosphate Phosphohydrolase (DIPP)."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AFZ646648; AAF74761.1; -.
EMBL; BC016534; AAH16534.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 AA; 19029 MW; E543BE5CBE520910 CRC64;
           303 AA; 35035 MW; D10EA8AAFE1D6705 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 AA.
                                                                                                                                                                  168 AA.
                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1928484; Nudt3.
Interpro; IPR000086; NUDIX_hydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00293; NUDIX; 1.
PRINTS; PR00502; NUDIXFAMILY.
PROSITE; PS00893; NUDIX; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=UTERUS;
MEDLINE=99043866; Pubmed=9822604;
                                                                                                                                                                  PRT;
                                      53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                            8; Conservative
                                                                                                                                                                   PRELIMINARY;
                                                                                                          204 KKSKSVDLPGDLFLN 218
                                                                                   1 KASQSVDYDGDSYMN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KASQSVDYDGDSY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 KSNOTRTYDGDGY 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                              Mus musculus (Mouse).
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                                                  Best Local Similarity
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      Complete proteome. SEQUENCE 303 AA;
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                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                 TISSUE=HEART;
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                                        Query Match
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Q9JI46;
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                                                               Matches
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                                                                                                                                                                                                                                     δλ
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STRAIN-PAOl;
Gagnon L.A., Castro-Urbina I.M., Liao X., Hancock R.E.W., Clarke A.J.,
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Safrany S.T., Caffrey J.J., yang X., Bembenek M.E., Moyer M.B., Burkhart W.A., Shears S.B.; "A novel context for the 'Mutr' module, a quardian of cell integrity, in a diphosphoinositol polyphosphate phosphohydrolase."; EMBO J. 17:6599-6607(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and characterization of PBD5 of Pseudomonas aeruginosa.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF147448; AAD32232.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.9%; Score 41; DB 2; Length 336; 54.5%; Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.9%; Score 41; DB 4; Length 172; 53.8%; Pred. No. 29;
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                                                                                                                                                                                                                                    Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF062539; AAC83225.1;
EMBL; AF062529; AAC83224.1;
EMBL; BC007727; AAH07727.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
1DAFBE8991787BBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 AA; 19471 MW; DE823FECF5C6438A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEWBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Membrane-bound lytic transglycosylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Membrane-bound lytic transglycosylase precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                               07727; AAH07727.1; -. IPR000086; NUDIX_hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00502; NUDIXFAMILY.
PROSITE; PS00893; NUDIX; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 29 PC
336 336 PC
336 AA; 37423 MW;
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GN MLTB2 OR PA4001.

S Pseudomonas aeruginosa.

C Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

C Bacteria; Proteobacteria; gamma subdivision; Pseudomonas aeruginosa.

OX NCBL_TaxID=287;

RN MCBL_TAXID=287;

RN STAIN-ATCC 15692 / PAO1;

RN MEDLINE-2043737; PubMed=10984043;

RN MEDLINE-2043737; PubMed=10984043;

RN MEDLINE-2043737; PubMed=10984043;

RN MEDLINE-2043737; PubMed=10984043;

RN AGARDER RL., COLIFY L., TOLENTINO E., Westbrock-Wadman S., Yuan Y., Canber R. L., Collty L., Tolentino E., Westbrock-Wadman S., Yuan Y., RA Garber R. L., Collty L., Tolentino E., Westbrock-Wadman S., Yuan Y., RA Garber R. L., Collty L., Tolentino E., Westbrock-Wadman S., Yuan Y., RA Garber R. L., Saler M.H., Hancock R.E.W., Kas A., Larbig W. Lim R.W., R. Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

RY "Complete genome sequence of Pseudomonas aeruginosa PAO1, an R. DR HSSP, P44025; Iurw.

Complete proteome.

SEQUENCE 340 AA; 37867 MW; 7AOOBD23AO695BD8 CRC64;

Query Match

Best Local Similarity 54.5%; Pred. No. 63; Length 340;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 SVDYDGDSYMN 15

11:1| ::| | ::| | ::| |

Db 208 AVDFGGGHIN 218

Search completed: February 14, 2003, 11:18:41
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(without alignments)
49.176 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                          al number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                    908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maximum Match 100%
Listing first 45 summaries
                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                            1 AASNLES 7
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220:
221:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	MAD 3B9 light chai	Anti-Fas MAb HFE7A	CDR of the light c	Light chain CDR fo	Mouse anti-Fas ant	Murine anti-Fas an	Antibody 4H5 L cha	Murine CD4/CD34 re	Mouse AC10 antibod	Humanised anti-Fas
SUMMARIES		ID	AAR70196	AAW83028	AAY23773	AAY18115	AAB14745	AAW90895	AAY59260	AAY51137	AAU99854	ABB74864
			16	19	20	20	21	21	21	21	23	23
		Query Match Length DB	7	7	7	7	7	7	7	7	7	7
	ф	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
		Score	31	31	31	31	31	31	31	31	31	31
		Result No.		2	m	4	5	9	7	80	0	10

Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived

Humanised anti-Fas	e Kappa III 1	antibody		Antibody 4H5 L cha	Murine derived pro	light	Light chain amino		Mouse anti-HIV mu5	Mouse-human chimer	Anti HIV antibody	Chimeric anti HIV	Light chain variab	Light chain sequen	Antibody 4H5 L cha		Murine derived pro	Mouse AC10 antibod		σ		ids				anti	ole ka	chain	Light chain variab	chain	chai	MAb 3E	cha	Light chain sequen	
ABB74910	2	AAR66144	Н	AAY59263	AAY51140	AAR33309	AAY85197	AAP90541	AAR55123	AAR55127	AAR60302	AAR60306	AAY23781	AAY18123	AAY59267	AAY51144	AAY51146	AAU99852	AAR24575	AAB71895	AAR04134	AAP90543	AAR04132	AAR32123	AAR75355	AAR70202	AAW34516	AAY23779	AAY23771	AAY18126	AAY18118	AAR70189	376	312	
23	23	15	21	21	21	14	21	10	1.5	15	15	15	20	20	21	21	21	23	13	22	11	10	11	14	16	16	18	20	20	20	20	16	20	20	
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11	12	13	14	15	9	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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Chimeric antibody; humanized antibody; antibody engineering; monoclonal antibody; MAb; interleukin-4; IL-4; allergy; CDR; complementarity determining region.
                                                                                                                                                                                                                                                           Gross MS, Holmes SD, Sylvester DR;
        AAR70196 standard; Protein; 7 AA.
                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                            93US-0136783.
                                                                                                                                                                                94WO-US10308
                                                                                                                                                                                                   93US-0117366
                                             20-SEP-1995 (first entry)
                                                                MAb 3B9 light chain CDR
                                                                                                                                                                                                                                                                              WPI; 1995-123387/16.
                                                                                                                                                                                07-SEP-1994;
                                                                                                                                                                                                    07-SEP-1993;
                                                                                                                                                                                                              14-OCT-1993;
                                                                                                                                                            16-MAR-1995.
                                                                                                                                            WO9507301-A.
                           AAR70196;
                                                                                                                          Mus sp.
AAR70196
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                                                                            Spleen cells from mice immunized with human IL-4 were used to prepare hybridomas, which were screened for anti-IL-4 MAD secretion. Only clone 3B9 was positive. CDNA clones of the 3B9 light and heavy chains were cloned into pGDN7+ and transformed into E. coli DH5-alpha. A light chain CDNA clone was sequenced (AAQ03490) that encoded the protein given in AAR70189. 3 CDRs (AAR70195-97) were
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apoptosis; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; solgerens syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atcpy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy; complementarity determing region;
                                                                                                                                                                                                                                                                                  ;
 from high affinity mAbs - useful in treatment of IL-4-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
                                                                                                                                                                                                                                              100.0%; Score 31; DB 16; Length 7; 100.0%; Pred. No. 7.8e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jun O, Kimihisa I; , Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-Fas MAb HFE7A light chain CDR-L2.
                 and IgE-mediated allergic conditions
                                               Disclosure; Page 55; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nobufusa S, Shin Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 185; 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          AAW83028 standard; Peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hideyuki H, Hiroko Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98AU-0059701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97JP-0082953
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                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
                                                                                                                                                                                                              7 AA;
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| AASNLES 7
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                                                                                                                                                                               identified.
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                                                                                                                                                                                                                 Seguence
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                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
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Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rhintis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
This is the amino acid of complementarity determining region 2 (CDR.L2) of the light chain (see AAW83042) of murine anti-human Fas monoclonal antibody HFBTA. The invention relates to antibodies, especially humanised antibodies (see AAW83031-37), recognising the Fas antigen. Such antibodies preferably comprise a heavy chain and a light chain including CDRs (see AAW83024-29) from the heavy and light chains of HFETA. Humanised antibodies are produced by CDR
                                                                                                                          grafting. The antibodies are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia,
                                                                                                                                                                                                                                                                                                                                     allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                           Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA molecules encoding recombinant antibodies useful for treating {\rm LL4\text{-}mediated} conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 31; DB 19; Length 7; 100.0%; Pred. No. 7.8e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDR of the light chain variable region of antibody 3B9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              allergy; complementarity determining region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY23773 standard; Peptide; 7 AA.
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93US-0117366.
93US-0136783.
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7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               7 AA;
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14-OCT-1993;
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Query Match
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                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody; interleukin-4; II4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease; complementarity determining region; CDR.
                                             The present sequence represents a complementarity determining region (CDR) of the light chain variable region of murine interleukin-4 (IL-4) antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunosjobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, hoper-versus-graff disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                         100.0%; Score 31; DB 20; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Light chain CDR for hIL-4 specific antibody.
                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                Example 3; Column 43-44; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sylvester DR;
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                                                                                                                                                                                                                                        endogenous IL-4 levels in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY18115 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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93US-0117366.
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                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-370482/31
                                                                                                                                                                                                                                                                                                             lery Match
let Local Similarity
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                                                                                                                                                                                                                                                                           7 AA;
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14-OCT-1993;
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conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   murine; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; artopy; arteriosclerosis; myocarditis; cardiomyoathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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100.0%; Pred. No. 7.8e+05;
tive 0; Mismatches 0;
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0
                                                                                                                                                                                                                            100.0%; Score 31; DB 20; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse anti-Fas antibody HFE7A light chain CDR2.
                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 65; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB14745 standard; peptide; 7 AA.
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Matches 7; Conservative
                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100..
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                                                                                                                                                                  7 AA;
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This invention describes a mover immensive anti-reas autoboy-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ilgand system, by binding to Fas on the cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents competed its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, anti-anemic, nephrotropic, anti-inflammatory, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic versus host disease, Sjorgen's syndameatoid arthritis, graft versus host disease, Sjorgen's syndameatoid arthritis, graft anemia, Addison's disease, relationable permittions or hypoplastic anemia, addison's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, alomerulonephritis, hepatitis (fulminant, chronic, viral (B). C or D) or alcoholic), and transplant rejection. (I) selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in
                                                                                                                                                                                                                                                                                                                                      Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic; anti-alergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyrominetic; antimentic; antinephrotropic; antinfertility; neuroprotective; antiatrerlosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia, Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple soclerosis; basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New humanized anti-Fas antibody, useful for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel humanized anti-Fas antibody-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakahara K, Tamaki I, Takahashi T;
                                                                                                                                                                                                                                                                                                  Murine anti-Fas antibody peptide fragment #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 98; 263pp; English.
                                                                                                                                                          AAW90895 standard; peptide; 7 AA.
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98JP-0276882.
                                                                                                                                                                                                                                                  08-AUG-2000 (first entry)
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                                          1 AASNLES 7
  AASNLES
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30-SEP-1998;
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                                                                                                               RESULT 6
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murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a murine anti-Fas antibody peptide fragment described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. Sequences AAX59259-61 represent the complementarity determining region (CDR)-1, CDR-2 and CDR-3 fragments in the L chain variable region of the
                                                                                                                                                 Gaps
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                                                                                                                     Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An antibody and the nucleic acid coding the antibody
                                                                                                                                                                                                                                                                                                                                                               Antibody 4H5 L chain variable region CDR2 fragment.
                                                                                                                                                                                                                                                                                                                                                                                            CD4 antigen; anti-human; antibody; 4H5; drug; CDR;
                                                                                                                  100.0%; Score 31; DB 21; 100.0%; Pred. No. 7.8e+05;
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                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            complementarity determining region.
                                                                                                                                                                                                                                                                           AAY59260 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                   17-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody 4H5 respectively.
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                                                                                       7 AA;
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                                                                                        Seguence
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                                                                                                                   Query Match
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AAY59260
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                                     Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived complementarity determining region CDR-2 protein fragment which is used to illustrate the method of
                                                                                                                                                                                                                                                                                                                                                                                                     Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells
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           Murine CD4/CD34 recognizing antibody light chain CDR-2 region #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hodgkin's Disease, mouse, AC10 antibody, light chain CDR, complementarity determining region.
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                                                                                                                                                                                                                                                                                                                                             Ono M, Soka T, Morimoto I, Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 77; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU99854 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                            (ASAH ) ASAHI KASEI KOGYO KK.
(ASAH ) ASAHI MEDICAL CO LTD.
                                                                                                                                                                                                                                                              98JP-0163023
                                                                                                                                                                                                                 99WO-JP02711
                                                                                                                                                                                                                                                 98JP-0159957
                                                                                         CDR-2; light chain; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-0CT-2002
                                                                                                                                                                                                                 24-MAY-1999;
                                                                                                                                                    WO9961629-A1
                                                                                                                                                                                                                                                              26-MAY-1998;
                                                                                                                                                                                   02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sednence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                        Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tches
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06-JUN-2002

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The invention describes an antibody (I) that immunospecifically binds to CD30, exerts a cytostatic or cytotoxic effect on Hodgkin's Disease cell line, and is not monoclonal antibody Ac10 or HeFi-1 and does not result from cleavage of Ac10 or HeFi-1 with papain or pepsin. (I), a protein (II) that competes for CD30 binding with the monoclonal antibodies Ac10 or HeFi, or exerts a cytotoxic or cytostatic effect on a Hodgkins' Ac10 disease cell line and the nucleic acid encoding the protein (III) are useful for the treatment or prevention of Hodgkin's Disease in a subject, by administering (I) to the subject, in the absence of conjugation to a cytostatic or cytotoxic agent, respectively and a pharmaceutically acceptable carrier. This is the amino acid sequence of the mouse Ac10 antibody light chain complementarity determining region 2 (CDR2), a polypeptide that competes with AC10 for CD30 binding.
                                                                                                                                                                                         Novel antibody that immunospecifically binds to CD30, useful for treating Hodgkin's disease, exerts a cytostatic or cytotoxic effect on Hodgkin's Disease cell line, and is not monoclonal antibody AC10 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drug containing humanised anti-Fas antibody, used for preventing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
light chain subunit; apoptosis; immunosuppressive; antiallergic;
autoimmune disease; allergy; atopic.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 31; DB 23; Length 7; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanised anti-Fas antibody related peptide SEQ ID NO 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                              Siegall CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                              Wahl AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB74864 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                               Claim 9; Page 99; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-2000; 2000JP-0090918.
                                                                            (SEAT-) SEATTLE GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAR-2001; 2001JP-0093106.
                                               28-NOV-2000; 2000US-0724406.
            28-NOV-2001; 2001WO-US44811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Best Local Similarity 100...
7; Conservative
                                                                                                               Risdon G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SANY ) SANKYO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-145113/19.
                                                                                                                                               WPI; 2002-557522/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 AA;
                                                                                                                                                                N-PSDB; ABK88126
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                                                                                                                 Francisco JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB74864
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                                                                                            caused by abnormality in Faryers ligand system containing as the active component an antibody having as the light chain subunit a polypeptide component an antibody having as the light chain subunit a polypeptide containing residues 1-218 of one of 3, 239 residue amino acid sequences, or residues 1-451 of one of 3, 470 residue amino acid sequences, all fully defined in the specification and having an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has immunosuppressive and antiallergic activity and is used for preventing and treating autoimmune diseases, allergy alopy and others. The present sequence is that of a peptide, useful to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a preventive or treating agent for diseases caused by abnormality in the Fas/Fas ligand system containing, as the active component, an antibody having a light chain subunit and a heavy chain subunit and a activity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has antiallergic, immunosuppressive and apoptotic activity and is used for preventing and treating autoimmune diseases, allergy, atopy and others. The present sequence is that of a peptide useful to the
                                                                              The invention relates to a preventive or treating agent for diseases
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;
heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic;
autoimmune disease; allergy; atopy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drug for preventing or treating e.g. autoimmune disease or allergy, comprises humanised anti-Fas antibody \,
                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 31; DB 23; Length 7; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised anti-Fas antibody related peptide SEQ ID NO 27.
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
  treating autoimmune diseases, allergy, and atopy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 6 (preparatory); Page 26; 154pp; Japanese.
                                       Example 6 (Preparatory); Page 26; 194pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB74910 standard; Peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2001; 2001JP-0093243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-APR-2002 (first entry)
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Best Local Similarity الاس..
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SANY ) SANKYO CO LTD.
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                                                                                                                                                                                                                                                                                                                7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AASNLES 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AASNLES 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB74910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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100.0%; Score 31; DB 23; Length 7;

Query Match

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The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynucleotides encoding different immunoglobulin binding protein (198P) polypeptides that specifically bind to a ligand or form one or more disulphide bonds that specifically bind to a ligand or form one or more disulphide bonds that specifically bind to a ligand or form one or more disulphide bonds to binds to a ligand, and transfermed plant cells are selected, and preparing an ighe array in plant cells. At least one peptide sequence has at least 75% sequence identity to a framework region (FR) of a native of 19M, 19G, 19A, 19D, 19E, 19Y, kappa or lambda immunoglobulin molecule. The method is useful for preparing an immunoglobulin binding protein array, preferably heavy chain binding protein (CHBP) array in eukaryotic cells (e.g. Agrobacterium tumefaciens or maize) or other cukaryotic cells (e.g. insect cells or mammalian cells). The CHBP is useful for discovery of e.g. screening assays of 19BPs having desired characteristics. The present sequence is a mammalian control or immunoglobulin derived peptide that may be incorporated into an 19BP of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding protein polypeptides specific to ligand, selecting plant cells for preparing array.
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                  0;
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0
                                                                                                                                                                                                                                                                                                                                           Immunoglobulin; antibody; light chain; heavy chain; CDR; FR. complementarity determining region; framework region; IgBP; transgenic plant; immunoglobulin binding protein array; IgM; IGG; IGA; IGD; IGE; IGY; IGM; Kappa; lambda; CHBP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 31; DB 23; Length 7; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
                                  Indels
           Pred. No. 7.8e+05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 14; 129pp; English.
100.08; Pre-
                                                                                                                                                                                               AAU70353 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                            Mouse Kappa III light chain CDR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAY-2000; 2000US-0563222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-2001; 2001WO-US14349.
                                                                                                                                                                                                                                                                    14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIC-) EPICYTE PHARM INC.
             Best Local Similarity 100. Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100...
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hiatt AC, Hein MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AA;
                                                                   1 AASNLES 7
                                                                                        1 AASNLES 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200183806-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AASNLES 7
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-2001.
                                                                                                                                                                                                                                    AAU70353;
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                                                                                                                                                             RESULT 12
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103 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-1998;
       30-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                17-APR-2000
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                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                               AAY59263;
                                           Muller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus sp.
                                                                                                                                                                                                                                                                                                                             RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1F7 antibody; murine; monoclonal antibody; diagnosis; HIV; infection;
AIDS; anti-HIV; human immunodeficiency virus; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1F7 antibody variable light chain L2 amino acid sequence SEQ ID NO:6
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                             AAR66140-R66146 are peptides complementary to the variable region
                                                                                                                                                                                                                                                                                                                     of the CD-4 antibody, these peptides are fixed onto a claimed nonwoven fabric (average fibre dia. of 1-30 microns) coated with seto-alkyl halide functional groups. This material can be used as a filter for CD-4 positive cells in a medical treatment involving the extra-corporeal circulation of blood.
                                                                                                                                                                                                                                                                Material for collecting cells positive for CD-4 antibody - comprises nonwoven fabric having keto-alkyl halide functional gp
                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 31; DB 15; Length 15; 100.0%; Pred. No. 2.2; ive 0; Mismatches 0; Indels
                                                                                                         CD-4 antibody variable region; complementary peptide; extra-corporeal blood circulation; cell filter material.
                                                                                        CD-4 antibody variable region complementary peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY91015 standard; protein; 41 AA.
                                    AAR66144 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                             Example 2; Page 7; 9pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0984277
                                                                                                                                                                                                             93JP-0057206
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100..
"...a 7; Conservative
                                                                        12-JUL-1995 (first entry)
                                                                                                                                                                                                                                                 WPI; 1994-346316/43.
                                                                                                                                                                                                                               (TOYM ) TOYOBO KK.
                                                                                                                                                                                                                                                                                                                                                                            15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AASNLES 15
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                                                                                                                                                       JP06269663-A
                                                                                                                                                                                           17-MAR-1993;
                                                                                                                                                                                                             17-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6057421-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-2000.
                                                                                                                                                                         27-SEP-1994.
                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY91015;
                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                        AAR66144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY91015
                              AAR66144
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The present invention describes the variable heavy and light chain regions (I) of murine monoclonal antibody (mAB) 1F7. AAY91014 to AAY91016 represent specifically claimed amino acid sequences of the variable light chain, and AAY91017 to AAY91019 represent specifically claimed amino acid sequence of the variable heavy chain. The antibodies are used for treatment of HIV (human immunodeficiency virus) infection and AIDS (acquired immunodeficiency syndrome). They are also used for committed is serial and for stimulating HIV antigen related and committed B cells to produce broadly reactive and neutralising antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the L chain variable region of the antibody 4H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                             Variable heavy and light chain regions of murine monoclonal antibody 1F7, useful for treating HIV infection and AIDS \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD4 antigen; anti-human; antibody; 4H5; drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY59263 standard; protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 8; 45pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98JP-0163034.
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94US-0351193
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                                                            (IMMP-) IMMPHERON INC.
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Sequence 16, p
Sequence 73, p
Sequence 73, p
Sequence 14, p
Sequence 2, Af
Sequence 2, Af
Sequence 2, Af
Sequence 2, Af
Sequence 75, p
Sequence 75, p
Sequence 24, p
Sequence 24, p
                                                                                                                      February 14, 2003, 11:13:07; Search time 6.32258 Seconds (without alignments) 32.575 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-483-632-18

US-08-481-651-6

US-08-466-151-6

US-08-461-181-6

US-08-491-845-16

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US-08-483-636-14

US-08-483-636-14

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US-08-483-632-14

US-08-859-939-3

US-08-859-93-3

US-08-579-378A-14

US-08-579-378A-14

US-08-579-378A-14

US-08-579-378A-14

US-08-579-378A-14

US-08-579-378A-14

US-08-579-378A-14

US-08-589-939-3

US-08-579-378A-18

US-08-579-378A-18

US-08-579-378A-18

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US-08-650-262-11

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US-08-137-117D-137
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                                                                                                                                                                                                                                                                                                                                                              262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 1008
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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STATE: Virginia COUNTRY: U.S. ZIP: 22314
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APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: STYLESTER INVESTER.
TITLE OF INVENTION: Recombinant IIA Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                    100.0%; Score 31; DB 2; Length 7; 100.0%; Pred. No. 1.9e+05; Live 0; Mismatches 0; Indels
                                                                             Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLING DATE:
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property Treffice. Box 1539 / UW2220 CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-0CT-1993
FILING DATE: 14-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-5EP-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P50186-3
                                                                                                                                                                                                                                         ; Sequence 18, Application US/08483632
; Patent No. 5928904
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,
                 Query Match
Best Local Similarity luv..
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Matches 7; Conservative
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; MOLECULE TYPE: protein
US-08-483-632-18
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GY: linear
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ZIP: 19406-0939
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US-08-483-636-18
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APPLICANT: Kohler, Heinz
TITLE OF INVENTION: VARIABLE HEAVY AND LIGHT CHAIN REGIONS OF MURINE
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1F7
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FLICATION NUMBER: US/08/984,277
FLILOS DATE: 3-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INCOMPATION:
NAME: PLOCE | PC-100 | PC-100 | PC-100 |
NAME: PLOCE | PC-100 | PC-100 | PC-100 |
NAME: PLOCE | PC-100 | PC-100 | PC-100 |
NAME: PLOCE | PC-100 | PC-100 | PC-100 |
NAME: PLOCE | PC-100 | PC-100 | PC-100 |
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
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APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
WUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                      STREES: McDermott, Will & Emery STREET: 99 Canal Center Plaza, Suite 300 CITY: Alexandria STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bucca, Daniel
REGISTRATION NUMBER: 42,368
REFERENCE/DOCKET NUMBER: 50200-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
Sequence 6, Application US/08984277
Patent No. 6057421
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-466-151-6; Sequence 6, Application US/08466151; Patent No. 6037453; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-756-8600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 41 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-756-8699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDermott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
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APPLICANT: KIMACHI, Kazuhiko
APPLICANT: BDA, Yasuhiko
APPLICANT: SHIOSAKI, Kouichi
APPLICANT: OSATOMI, Kiyoshi
APPLICANT: OSATOMI, Sachio
TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/491,845
                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 419 Seventh Street N.W. Ste. 300 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00039
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: MAEDA=5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/08491845
Patent No. 5773247
GENERAL INFORMATION:
APPLICANT: MAEDA, Hiroaki
                                                                                                                      Sequence 8, Application US/08491845
Patent No. 5773247
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    Browdy and Neimark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Browdy, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIMACHI, Kazuhiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 111 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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1 AASNLES 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20004
                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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APPLICANT:
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                                                                                    RESULT 6
US-08-491-845-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 31; DB 3; Length 106; 100.0%; Pred. No. 4.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

PPPLICANT: Jardieu, Paula M.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1

CURRENT APPLICATION NUMBER: US/08/466,163B

CURRENT FILING DATE: 1995-06-06

PRIOR APPLICATION NUMBER: US 08/185,899

PRIOR FILING DATE: 1995-03-15

PRIOR FILING DATE: 1994-01-26

PRIOR FILING DATE: 1994-01-26

PRIOR FILING DATE: 1994-01-26

PRIOR FILING DATE: 1994-01-76

PRIOR FILING DATE: 1994-01-76

PRIOR FILING DATE: 1994-01-76

PRIOR FILING DATE: 1991-08-07

NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: SVODDGA, CTAIG G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
TELEPAN: 650/225-1489
TELEPAN: 650/225-1489
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
  SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08466163B Patent No. 6329509
                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/185899 FILING DATE: 26-JAN-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/879495 FILING DATE: 07-MAX-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/744768 FILING DATE: 14-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-7un-1995
APPLICATION NUMBER: 08/405617
                                                                                                                                                                       UMBER: 08/405617
15-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

Best Local Similarity 100.0

Matches 7; Conservative
                                                                                                                                                                                             FILING DATE: 15-MAR-1 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Mus musculus
US-08-466-163B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AASNLES 7
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US-08-466-163B-6
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Gaps ; Query Match 100.0%; Score 31; DB 1; Length 111; Best Local Similarity 100.0%; Pred. No. 4.5; Matches 7; Conservative 0; Mismatches 0; Indels APPLICANT: TOKIYOSHI, Sachio TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND APPLICANT: EDA, Yasuyuki APPLICANT: SHIOSAKI, Kouichi APPLICANT: OSATOMI, Kiyoshi APPLICANT: TOKIYOSHI, Sachio

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APPLICATION NUMBER: US 08/11/366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                   P50186-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 73, Application US/08483632
Patent No. 5928904
GENERAL INFORMATION:
                                                                                                                                                                        FILING DATE: 07-SEP-1914
ATTORNEY/AGENT INFORMATION:
NAME: SULTON, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P5018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 111 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sutton, Jeffrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.C
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-483-636-73
                                                                                                                                                                                                                                                                                                                                                                                                                                         single
      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 19406-0939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESSONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITT. King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 31; DB 1; Length 111; 100.0%; Pred. No. 4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/491,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/483,636
                                                              ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00039
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25.618
REFERENCE/DOCKET NUMBER: MAEDA-5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 73, Application US/08483636 Patent No. 5914110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 111 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-491-845-16
                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENERAL INFORMATION:
                                                                                                                                                   USA
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                                                                                                                               D.C.
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                                                                                                                           STATE: D
COUNTRY:
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Gaps
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100.0%; Score 31; DB 2; Length 111; 100.0%; Pred. No. 4.5; Uive 0; Mismatches 0; Indels
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APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders ON SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE: CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/11/366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 / UW2220 CITY: King of Prussia
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100.0%; Score 31; DB 3; Length 115; 100.0%; Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/483,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                Sequence 14, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
Query Match
Best Local Similarity luv...
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Best Local Similarity 100.

Matches 7; Conservative
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 AASNLES 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                            58 AASNLES 64
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                                                                                          1 AASNLES 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PA
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                                                                                                                                                                                                   US-08-483-636-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
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100.0%; Score 31; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                 REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,968
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 78913/1993
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 51, Application US/08513968 Patent No. 6114143 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: ED
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 248633
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OSATOMI, KIYOSHI
APPLICANT: KIMACHI, KAZUHIKO
APPLICANT: HIGUCHI, HIROFUMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAEDA, Hiroaki
MAKIZUMI, Kelichi
SHIOSAKI, Kouichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 202-628-5197
202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDA, Yasuyuki
                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-513-968-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                        1 AASNLES 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-513-968-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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Gaps
0
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                                                                                                                                                                                                                                                                                                                             APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 14-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTONNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sutton, Jeffrey A.
RECISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 58, Application US/08483636
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us-09-701-001b-5.rai

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Query Match 100.0%; Score 31; DB 2; Length 131; Best Local Similarity 100.0%; Pred. No. 5.4; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 19406-0039
ZIP: 19406-0039
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/483,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SmithKline Beecham Corp./Corporate
                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
ATTORNEY AGENT INFORMATION:
NAME: SULLON, Jeffrey A.
REGISTRATION NUMBER: 34,028
REGISTRATION NUMBER: 94,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 58, Application US/08483632; Patent No. 5928904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
     King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-483-632-14
                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 AASNLES 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AASNLES 7
                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: K
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bst Local Similarity 100.0%; Pred. No. 5.4;
atches 7; Conservative 0; Mismatches 0; Indels
GENERAL INCORMATION:
GENERAL INCOMMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKilne Beecham Corp./Corporate ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
                                                                                                                                                            CORRESPONDENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 / UW2220 CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/11/366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION NUMBER: US 08/136/783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
RILING DATE: 07-SEP-1994
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT/US/94/10308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: P50186-3 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-483-632-14; Sequence 14, Application US/08483632; Patent No. 5928904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 131 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-483-636-58
                                                                                                                                                                                                                                                                                                                                                               ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Gaps

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APPLICANT: Hackett, Jr., John R.
APPLICANT: Hoff, Jane A.
APPLICANT: Ostrow, David H.
APPLICANT: Golden, Alan M.
TITLE OF INVENTION: CONTROLS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSE: Abbott Laboratories
STREET: 100 Abbott Park Road
COTTY: Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 31; DB 2; Length 131; Best Local Similarity 100.0%; Pred. No. 5.4; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,939
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 5865.US.01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 198-2623
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILLING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILLING DATE: 14-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATPLICATION DATA:
ATPLICATION DATA:
ATPLICATION DATA:
ATPLICATION DATA:
ATPLICATION DATA:
ATPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                             NAME: SULTON, JEffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEPHONE: (215) 270-5090
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-08-589-939-3
; Sequence 3, Application US/08589939
; Patent No. 6015662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 131 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-483-632-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 AASNLES 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AASNLES 7
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-589-593-3
Query Match
Best Local Similarity 100.0%; Score 31; DB 3; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AASNLES 7
Oy 1 AASNLES 7
Search completed: February 14, 2003, 11:20:50
JOb time: 7.3258 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 14, 2003, 11:15:53; Search time 4.06452 Seconds (without alignments) 44.001 Million cell updates/sec Run on:

US-09-701-001B-5

1 AASNLES 7 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

140259 segs, 25548876 residues arched:

lotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000300000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database

Published_Applications_AA:*

1. / cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep: *
22. / cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep: *
33. / cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep: *
34. / cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep: *
35. / cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep: *
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39. / cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep: *
39. / cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep: *
39. / cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep: *
39. / cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep: * 9. 110: 112: 14:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 18, Appl	Sequence 0, Appli Sequence 6, Appli	Sequence 14, Appl	Sequence 58, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 93, Appl	Sequence 95, Appl	Sequence 19, Appl	Sequence 20, Appl	Sequence 80, Appl	Sequence 81, Appl	Seguence 84, Appl	Sequence 85, Appl	Sequence 86, Appl	Sequence 94, Appl	Sequence 36, Appl
B ID	9 US-09-879-461-18	10 US-09-802-096-6	9 US-09-879-461-14	9 US-09-879-461-58	9 US-09-879-461-2	10 US-09-917-410-2	9 US-09-903-327A-4	9 US-09-144-886-93	9 US-09-144-886-95	10 US-09-839-447A-19	10 US-09-839-447A-20	9 US-09-144-886-80	9 US-09-144-886-81	9 US-09-144-886-84	9 US-09-144-886-85	9 US-09-144-886-86	9 US-09-144-886-94	10 US-09-810-502-36
% Query Match Length DB	7	106	131	131	132	218	238	111	112	20	20	112	112	112	112	112	112	112
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	90.3	90.3	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1
Score	31	31	31	31	31	31	31	28	28	27	27	27	27	27	27	27	27	27
Result No.	1	9 M	4	Ŋ	φ	7	ω	σ	10	11	12	13	14	15	16	17	18	19

NAME: SULLON, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFRENCE/DOCKET NUMBER: 950186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:

Sequence 37, Appli Sequence 2, Appli Sequence 12, Appli Sequence 7, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 14, Appli Sequence 14, Appli Sequence 16, Appli Sequence 16, Appli Sequence 116, Appli Sequence 116, Appli Sequence 1116, Appli Sequence 1117, Appli Sequence 1118, Appli Sequence 1184, Appli Sequence 185, Appli Sequence 186, Appli Sequence 186, Appli Sequence 186, Appli Sequence 186, Appli Sequence 186, Appli	Uw2220 - 709
US-09-810-502-37 US-09-839-447A-2 US-09-800-065-2 US-09-920-171-7 US-09-920-171-7 US-09-956-086-3 US-09-956-086-3 US-09-956-087-3 US-09-986-442-6 US-09-987-686-7 US-09-981-132-333 US-09-864-761-38594 US-09-864-761-38594 US-09-864-761-38594 US-09-864-761-3959 US-09-864-1132-333 US-09-864-1132-333 US-09-864-1132-394 US-09-986-1118 US-09-986-1118 US-09-986-1118 US-09-986-1118 US-09-986-1118 US-09-986-1118 US-09-986-1118 US-09-986-1118 US-09-986-1118 US-09-981-1132-445 US-09-841-132-594 US-09-981-1132-98	ALIGNMENTS 61 S. S. In ant IL4 Antibodies nt of IL4 Mediated Beecham Corporation llectual Property, tible OS/MS-DOS ease #1.0, Version 01 wn> /09/879,461 wn> /612,929 08/136,783
112 10 619 10 108 10 108 10 1109 10 1109 10 263 9 283 10 283 10 554 10 875 10 894 9 894 9 894 9 894 9 894 9 894 9 894 9 894 9 894 9 894 9	on US/09 0193575A 019357A 01935
88 8 8 8 8 8 8 8 7 . 1 . 1 . 1 . 1 . 1 . 1 . 1 . 1 . 1 .	9-879-461-18 9-879-461-18 9-879-461-18 91-68 Application US/091 91-68 Application Wo. US20020193575A. GENERAL INFORMATION: TICANT: HOLMES, Mitch Sylvester, Daylester, Daylester, Daylester, Daylester, Daylester, Daylester, Dayles Correspondence Address: RADRESSEE: SmithKl. STREET: Corporate STATE: PA COUNTRY: USA COUNTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: FORM: MEDIUM TYPE: FORM: MEDIUM TYPE: FORM: MEDIUM TYPE: 12-JUU CURRENT APPLICATION DATA: RAPLICATION NUMBER FILING DATE: 12-JUU CLASSIFICATION DATA: RAPLICATION DATA: RAPLICATION DATA: RELING DATE: 14-OC' ATTORRAY INDERNAT
66666666666666666666666666666666666666	SSULT 1 S-09-879-461-18 Publication No GENERAL INFORM APPLICANT TITLE OF CORRESPON STRE COUN COUN COUN COUN COUN COUN COUN COUN
01000000000000000000000000000000000000	RESULT 0S-09-8 > Seque > Publi

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Gaps
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ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 - 709
STREET Swedeland RG.
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
Sylvester, Daniel R.
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
                                                                                                                                                                                100.0%; Score 31; DB 10; Length 106; 100.0%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 31; DB 9; Length 131; 100.0%; Pred. No. 3.2;
                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE: 12-Jun-2001
CLASSIFICATION: <URNOWN>
PRIOR APPLICATION: <URNOWN>
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                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/612,929
FILING DATE: CURKNOWN>
APPLICATION NUMBER: 05 08/136,783
FILING DATE: 14-0CT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P50186-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 131 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
      1991-08-14
                                                                                                                                                                                                    Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                            ; ORGANISM: Mus musculus
US-09-802-096-6
                      NUMBER OF SEQ ID NOS:
SEQ ID NO 6
LENGTH: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
    PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                               73 AASNLES 79
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                                                                                                                                                                                                                                                                                                                                                                                                US-09-879-461-14
                                                                                          TYPE: PRT
                                                                                                                                                                                Query Match
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Sequence 6, Application US/09802096

GENERAL INFORMATION:
APPLICANT: Breatu, Paula M.
APPLICANT: Bresta, Leonard G.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended FILE REFERENCE: PO718P2C3US
CURRENT APPLICATION NUMBER: US/09/802,096
CURRENT FILING DATE: 1094-01-308
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: PCT/VUS92/06860
PRIOR APPLICATION NUMBER: PCT/VUS92/06860
PRIOR APPLICATION NUMBER: US 08/495
PRIOR FILING DATE: 1992-08-114
PRIOR FILING DATE: 1992-08-10-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: US92-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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APPLICANTON: Method of Treating Allergic Disorders (as amended)
FILE REFERENCE: P0718P2C2US
CURRENT APPLICATION NUMBER: US/09/802,077
CURRENT FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: P07/US92/06860
PRIOR FILING DATE: 1994-01-26
PRIOR PILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR PILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
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                                                                                                                                                       Length 7;
                                                                                                                                                100.0%; Score 31; DB 9; I
ilarity 100.0%; Pred. No. 1.2e+05;
Conservative 0; Mismatches 0;
           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US 07/744,768
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09802077 Patent No. US20010033842A1
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                            Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AASNLES 7
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STREET: Corporate Intellectual Property, UW2220 - 709 Swedeland Rd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII, WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5" Computer Disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-879-461-2
                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/612,929
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Felfe & Lynch STREET: 805 Third Avenue
                                                                                              ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09917410 Patent No. US20020098183A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 132 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (215) 270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                             CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10022
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 7; Conserv
                                                                    STATE: PA
                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 AASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AASNLES 7
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0
                                                                                                                                                                                                                                                                         Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in Tratment of IL4 Mediated Disorders
                                                                                 Sequence 58, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 31; DB 9; Length 131; 100.0%; Pred. No. 3.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
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ADDRESSEE: SmithKline Beecham Corporation
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEPAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 58:
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APPLICATION NUMBER: 08/612,929
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
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NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
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Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: HOlmes, Stephen D.
Gross, Mitchell S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 131 amino acids
                                                                                                                                                                                                                                                                                                                                                           CITY: King of Prussia
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 19406-2799
                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                  STATE: PA
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                                                                       US-09-879-461-58
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MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR PREVENTION OF ACUTE ORGAN DAMAGE AFTER EXTRACORPOREAL BLOOD CIRCULATION
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TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
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Gaps

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0; Gaps
   APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Detulinum Neurotoxins
FITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2560.117050
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 93
LENGTH: 111
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APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Bottlinum Neurotoxins
FILE REFERENCE: 2500.117050
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT APPLICATION NUMBER: US/09/144,886
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone COTHER INFORMATION: 1C6 region VL epitope 3 US-09-144-886-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone CTHER INFORMATION: 1G5 region VL epitope 3 US-09-144-886-95
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85.7%; Pred. No. 12;
iive 1; Mismatches 0; Indels
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85.7%; Pred. No. 13;
1ive 1; Mismatches 0; Indels
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TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
FILE REFERENCE: TRIPEPP.0200P1
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; Patent No. US20020155114A1
                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 6; Conservative
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Best Local Similarity
'-hos 6; Conserva
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: LOCATION: (0)...(0)

: OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody

US-09-903-327A-4
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                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
                        APPLICATION NUMBER: 08/578,953
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020098183A1man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 218
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Best Local Similarity
Matches 7; Conserv
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US-09-903-327A-4
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US-09-144-886-93
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Search completed: February 14, 2003, 11:21:31
Best Local Similarity
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| 55 ASNLES 60
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                                                    2 ASNLES 7
                                                                                                                                               RESULT 14
US-09-144-886-81
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LENGTH: 112
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                   Matches
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Patent No. US20020155114A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Detulinum Neurotoxins
FILE REFERENCE: 2500.117080
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Sallberg, Matti
TITLE OF INVENTION: SYMHETIC PEPTIDES THAT BIND TO THE
TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
FILE REFERENCE: TRIPEP.020CP1
CURRENT APPLICATION NUMBER: US/09/839,447A
CURRENT APPLICATION NUMBER: 09/556605
PRIOR FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 20
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                                                                                                                                               DB 10; Length 20; 3.5;
                                                                                                                                                                                   0; Indels
                                                                                                                                               87.1%; Score 27; DB 100.0%; Pred. No. 3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION: Artificial Peptide US-09-839-447A-20
                                                                                          ; OTHER INFORMATION: Artificial Peptide US-09-839-447A-19
                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/09839447A Patent No. US20020058247A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                      TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity luv..
6; Conservative
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Best Local Similarity 100.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                 RESULT 12
-09-839-447A-20
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US-09-144-886-80
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LENGTH: 112
   SEQ ID NO 19
LENGTH: 20
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                                                                             FEATURE:
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                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize TITLE REPERENCE: 2500.117 USC CURRENT APPLICATION NUMBER: US/09/144,886 CURRENT FILING DATE: 1998-08-31 NUMBER OF SEO ID NOS: 98 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                  APPLICANT: Marks, James D
APPLICANT: Marks, James D
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117050
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SSOFTWARE: Patentin Ver. 2.0
SSOFTWARE: Patentin Ver. 2.0
LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone; OTHER INFORMATION: 1A1 region VL epitope 2 US-09-144-886-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone COTHER INFORMATION: 1C9 region VL epitope 1 US-09-144-886-81
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100.0%; Pred. No. 21;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 87.1%; Score 27; DB Best Local Similarity 100.0%; Pred. No. 21; Matches 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 84, Application US/09144886; Patent No. US20020155114A1; GENERAL INFORMATION:
APPLICANT: Marks, James D; APPLICANT: Amersdorfer, Peter
                                                                                                                                                                                                                                               ; Sequence 81, Application US/09144886
; Patent No. US20020155114A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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                            6; Conservative
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Best Local Similarity
Matches 6; Conserv
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Job time : 4.06452 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 14, 2003, 11:12:02; Search time 7 Seconds Run on:

(without alignments) 96.134 Million cell updates/sec

US-09-701-001B-5 Perfect score:

1 AASNLES 7

Sequence:

BLOSUM62 Scoring table:

283224 segs, 96134422 residues ched:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

PIR_73:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	kappa chair	kappa	Ig kappa chain pre	hypothetical prote	6-phosphofructokin	hypothetical prote	cold shock proteir	Ig kappa chain V-I	Ig kappa chain V r	pr	Ig kappa chain - h	hypothetical prote		hypothetical prote	capsomere protein	nonstructural prot		ATP-dependent zinc	nesin-r	Ig kappa								
ID	C38601	A38601	KVMS10	KVMSC1	KVMS43	KVMS83	KVMS69	S19971	S19976	PH1226	B64160	T39624	T00362	AH3440	K1HUGL	S19972	S06731	S40370	C87521	A98166	AF3121	OMXRWT	OMXRWN	AB2177	D71941	A55236	S42193	S25462
DB	200	4 (2	П	П		-	Н	7	7	7	7	7	7	~	-	7	7	7	7	~	7	, -1	-	7	7	Н	7	7
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	100	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		90.3		90.3	90.3		90.3		0	90.3	90.3		90.3		87.1
Score	31	31	31			31	31	31	31	31	31	31	31	28	28	28	28	28	28	28	28	28	28	28	28	28	27	27
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Ig kappa chain V r	light chain	light	light chain	kappa	kappa chain	kappa chain	kappa chain	kappa chain	kappa	kappa chain	kappa chain				
S25177	S59640	PH1076	PH1077	S26343	S26344	K1HUAU	KVMS54	KVMS37	KVMS08	KVMS84	KVMS75	KVMS40	809963	209965	996608
7	7	~	~	7	~	Н	Н	Н	Н	-	-		7	7	7
95	101	102	102	107	107	108	108	111	111	111	111	111	111	111	111
87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87.1	87 1

ALIGNMENTS

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C;Accession: C38601
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same anti-
                                                       Ig kappa chain V region (2B5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M57980; NID:g196406; PIDN:AAA63361.1; PID:g196407
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-65 <GOS>
                                                                                                                                                                                                                                                                                                                                                      A; Accession: C38601
RESULT 1
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Gaps . 0 Query Match 100.0%; Score 31; DB 2; Length 65; Best Local Similarity 100.0%; Pred. No. 0.87; Matches 7; Conservative 0; Mismatches 0; Indels

. 0

1 AASNLES 7 δy

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RESULT 2 B38601

Ig kappa chain V region (7D4) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 30-Aug.1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999

C. Accession: B38601
R. Goshorn, S.C.: Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A; Title: Common structural features among monoclonal antibodies binding the same anti
A; Reference number: A38601; MUID:91115823; PMID:1703527
A; Accession: B38601
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-65 <GOS>
A; Residues: 1-65 <GOS>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin

Gaps .. 0 Query Match 100.0%; Score 31; DB 2; Length 65; Best Local Similarity 100.0%; Pred. No. 0.87; Matches 7; Conservative 0; Mismatches 0; Indels

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RESULT 3

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A; McGesule type: protein
A; Residues: 1-111 < WEI>
Residues: 1-111 < WEI>
Residues: 1-111 < WEI>
Residues: 1-111 < WEI>
Rux. J. Immunol. 23, 2503-2510, 1993
A; Title: Variable region gene selection of immunoglobulin G-expressing B cells with s A; Reference number: S42176; MUID:94009207; PMID:7691608
A; Residues: 10-99 < WOJA
A; Residues: 12-99 < WOJA
A; Residues: 12-90 < WOJA
A;
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C; Superfamily: immunoglobulin V region; immunoglobulin homology
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A; Residues: 10-99 <MOO>
A; Residues: 10-99 <MOO>
A; Residues: 10-99 <MOO>
A; Residues: 10-90 <MOO>
A; Residues: 10-90 <MOO>
A; Cross-references: EMBL: Z25454; NID:9407842; PIDN:CAA80941.1; PID:9407843
A; Votes: V-kappa-21E; anti-collagen
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
distulfide bonds: In some cases, such as IgA and IgM, the subunits associate into
C; Superfamily: immunoglobulin hamnoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 16-94/Domain: immunoglobulin homology <IMM>
F; 16-94/Domain: immunoglobulin homology <IMM>
F; 23-92/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain V region (PC7043) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
C; Accession: A01937; S42187; S42199; S42199; S42199; S42191; S42192
R; Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A; Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A; Reference number: A93204; MUID:79073152; PMID:103003
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A;Residues: 10-99 <MOVY>
A;Cross-references: EMBL:225452; NID:g407840; PIDN:CAA80939.1; PID:g407841
A;Note: V'kappa-21E; anti-collagen
A;Accession: S42192
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A;Residues: 12-99 <MOZ>
A;Cross-references: EMBL:225446; NID:9407834; PIDN:CAA80933.1; PID:9407835
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                            100.0%; Score 31; DB 1; Length 111; 100.0%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                         C; Keywords: heterotetramer
F;16-94/Domain: immunoglobulin homology <IN
F;23-92/Disulfide bonds: #status predicted
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A; Accession: S42191
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A; Molecule type: DNA
A; Residues: 15-99 <MOA>
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100.0%; Score 31; DB 2; Length 93; 100.0%; Pred. No. 1.3;

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Local Similarity 100.

Query Match st Loca

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Ig kappa chain V region (PC7210) - mouse

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KVMSC1

Cy Accession: Was musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 31-Mar-2000
C; Accession: A01936
A; Title: Mochanisms of antibody diversity: multiple genes encode structurally related mcA; Reference number: A93822; MuID:79012520; PMID:99744
A; Accession: A01936
A; Molcoule type: protein
A; Residues: 1-111 cAMCK>
C; Comment: This chain was isolated from a myeloma protein.
C; Comment: This chain was isolated from a subunit consists of two identical light (kap
                                                                                                                                                                                   C. Accession: 30-Aug-1999
R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common Structural features among monoclonal antibodies binding the same antigen A:Title: Common structural features among monoclonal antibodies binding the same antigen A:Title: Common structural features among monoclonal antibodies binding the same antigen A:Tatle: Common structural features among monoclonal antibodies binding the same antigen A:Tatle: A:Recession: A38601
A:Reference number: A38601
A:Status: preliminary
A:Residues: 1-93 <GOS>
A:Cross-references: GB:M57978; NID:g196402; PIDN:AAA63359.1; PID:g196403
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
Ig kappa chain V region (1G3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
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Indels

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0; Mismatches

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Ouery Match st Local Similarity

100.0%; Score 31; DB 1; Length 110; 100.0%; Pred. No. 1.6;

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C;Accession: PH1226
R;Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; L
Gene 121, 271-278, 1992
A;Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and A;Reference number: PH1224; MUID:93077041; PMID:1446824
A;Accession: PH1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-131 <WEL>
A;Residues: 1-131 <WEL>
A;Cross-references: GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:g260766
A;Cross-references: GB:S50265; NiD:g260765; PIDN:AAB24320.1; PID:g260766
A;Note: this mouse sequence was hybridized and fused with a human constant region gen C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
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C; Species: Mus musculus (house mouse)
C; Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C; Accession: S19976
R; Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
R; Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
A; Description: Structural characterization of CD4 mAb.
A; Reference number: S19963
A; Accession: S19976
A; Molecule type: MRNA
A; Molecule type: MRNA
A; Residues: 1-112 < WEIS
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C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                           Submitted to the EMBL Data Library, March 1992
Algescription: Structural characterization of CD4 mAb.
A.Reference number: $19963
A.Reference number: $19971
A.Rolecule type: mRNA
A.Residues: 1-112 <WEI>
A.Cross references: EMBL:X65091; NID:952288; PIDN:CAA46219.1; PID:952289
A.Experimental source: clone M-T310
A.Accession: $19973
A.Residues: 1-112 <WENA
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Pred. No. 1.6;
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Best Local Similarity 100.v
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Best Local Similarity 10v..
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C; Accession: S19971; S19973
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A; Residues: 1-111 <WEI>
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappensistalide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology < IMM>
F; 16-94/Pomain: immunoglobulin homology < IMM>
F; 23-92/Disulfide bonds: #status predicted
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F;16-94/Domain: immunoglobulin homology <IMM>F;16-94/Domain: immunoglobulin homology <IMM>F;23-92/Disulfide bonds: #status predicted
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Nature 276, 785-790, 1978

tile: Rearrangement of genetic information may produce immunoglobulin diversity.

eference number: A93204; MUID: 79073152; PMID: 103003
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C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Mus musculus (house mouse)
C.Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C.Accession: B01937; A01937
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                                           100.0%; Score 31; DB 1; Length 111; 100.0%; Pred. No. 1.6;
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Best Local Similarity 100.v
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Best Local Similarity
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A; Molecule type: protein
A; Residues: 1-111 <WEI>
                                                                                  Best Local Similarity
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54 AASNLES 60
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C. Accession: T00362
R. Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, DNA Res. 5, 169-176, 1998
A.; Itle: Prediction of the coding sequences of unidentified human genes. X. The compl A; Reference number: Z14142; MUID:98403880; PMID:9734811
A. Accession: T00362
A.; Stelminary; translated from GB/EMBL/DDBJ
A.; Molecule type: mRNA
A.; Molecule type: mRNA
A.; Residues: 1-1208 < ISH-
A.; Cross references: EMBL:AB014575; NID:g3327163; PIDN:BAA31650.1; PID:g3327164
A.; Experimental source: brain; clone HK02566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cold shock protein cspa [imported] - Brucella melitensis (strain 16M)
C.Species: Brucella melitensis
C.Species: Brucella melita
R.Species: Brucella May-2002
R.Detamor, A.B. A.B. A.B. A.B. Beat, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
R.Delvechio, V.G.; Kapatral, V.; Redkar, R.J.; PH.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A.Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A.Reference number: AD3252; PMID:11756688
A.Status: preliminary
A.Status: preliminary
A.Status: Draliminary
A.Status: Brain Info
A.Cross-references: GB:ABD08917; PIDN:AAL52691.1; PID:g17983518; GSPDB:GN00190
A.Steperinental source: strain 16M
C.Gene: BMEIL510
                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 02-Sep-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 31; DB 2; Length 1208; Best Local Similarity 100.0%; Pred. No. 24; Matches 7; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: KIAA0675
C;Superfamily: RING finger homology
F;1144-1193/Domain: RING finger homology <RRN>
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Job time : 7 secs
                                                                               hypothetical protein KIAA0675 - human
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85.7%;
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Matches 6; Conservative
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| 62 AAANLES 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein H10852 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Species: B64160
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, R;Fleischmann, R.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Fritchman, J.L.; Glodek, A.; Kelley, J.M.; Weidman, M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Artitle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: B64160
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-463 <TIGR>
A;Crossreferences: GB:U32766; GB:L42023; NID:g1573854; PIDN:AAC22509.1; PID:g1573866; TA;Note: best homolog was a hypothetical protein from Escherichia coli
C;Superfamily: multidrug-efflux transporter
C;Keywords: antibiotic resistance; transmembrane protein
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A. Accession: T39624
A. Status: preliminary: translated from GB/EMBL/DDBJ
A. Molecule type: DNA
A. Residues: 1-942 < WOO>
A. Cross-references: EMBL. AL022104; PIDN:CAA17900.1; GSPDB:GN00067; SPDB:SPBC16H5.02
A. Experimental source: strain 972h-; cosmid c16H5
A. Genetics: SPBB:SPBC16H5.02
A. Genetics: SPBB:SPBC16H5.02
A. Map position: 2
C. Superfamily: human 6-phosphofructokinase; 6-phosphofructokinase 1 homology
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
                                                                                                                                                                                                                         Gaps
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Od, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
Mitted to the EMBL Data Library, March 1998
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F;1-20/Domain: signal sequence #status predicted <SIG>F;21-131/Product: Ig light chain V region #status predicted <MAT>F;36-114/Domain: immunoglobulin homology <IMM>
                                                                                                                                         100.0%; Score 31; DB 2; Length 131; 100.0%; Pred. No. 1.9; ative 0; Mismatches 0; Indels
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100.0%; Score 31; DB 2; Length 463;
Best Local Similarity 100.0%; Pred. No. 8;
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Score 28; DB 2; Length 69; Pred. No. 5.5; 1; Mismatches 0; Indels

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 14, 2003, 11:05:27 ; Search time 3.6129 Seconds (without alignments) 80.360 Million cell updates/sec Run on:

US-09-701-001B-5 31 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 AASNLES 7 Scoring table: Sequence:

112892 seqs, 41476328 residues ched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P01668 mus musculu	P01664 mus musculu	5 mus	P01666 mus musculu	5	P44903 haemophilus	_		_	Q9zm66 helicobacte	P46867 drosophila	P01594 homo sapien	P01674 mus musculu	P01660 mus musculu	P01662 mus musculu	P01663 mus musculu	P01667 mus musculu	P01670 mus musculu	P01671 mus musculu	P01672 mus musculu	_	P39823 bacillus su				Q928i0 listeria in	Q8y4i2 listeria mo	~		~1	halo	P01659 mus musculu	P01658 mus musculu
Communica	ID	KV3P_MOUSE	KV3L_MOUSE	KV3M_MOUSE	KV3N_MOUSE	KV3Q_MOUSE	YIEO_HAEIN	KV1G_HUMAN	VP9_WTV	VP9_WTVNJ	FTSH_HELPJ	KL68_DROME	KV1B_HUMAN	KV3V_MOUSE	KV3H_MOUSE	KV3J_MOUSE	KV3K_MOUSE	KV30_MOUSE	KV3R_MOUSE	KV3S_MOUSE	KV3T_MOUSE	KV3I_MOUSE	PSS_BACSU	CUT1_FUSSO	CUTI_FUSSC	UPPS_BACSU	PGK_LISIN	PGK_LISMO	YN8U_YEAST	- 1	UVRB_RICPR	UVRB_HALN1	KV3G_MOUSE	KV3F_MOUSE
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Q23983 drosophila P35790 homo sapien Q03100 dictyosteli Q99323 drosophila Q99718 natrialba m Q9pnj6 campylobact Q99626 homo sapien Q04649 mesocricetu O70367 rattus norv P05167 hordeum vul Q60013 streptomyce Q26327 methanobact	PRT; 110 AA. ted) . sequence update) . annotation update) n PC 7210. ta; Craniata; Vertebrata; Euteleostomi; .ia; Sciurognathi; Muridae; Murinae; Mus. 103003; Loh E., Schilling J., Hood L.E.; information may produce immunoglobulin	FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2. COMPLEMENTARITY-DETERMINING-2. COMPLEMENTARITY-DETERMINING-3. COMPLEMENTARITY-DETERMINING-3. BY SIMILARITY. 69F1A5CEB86B1249 CRC64;	; DB 1; Length 110; .0.86; O. Indels O; Gaps O;	PRT; 111 AA. quence update) notation update) SPC 101. Craniata; Vertebrata; Buteleostomi;
SNAP_DROME KICH_HUMAN CYAA_DICDI MYSN_DROME PLAZ_NATWA PYRB_CAMJE CDXZ_HUMAN CDXZ_HUMAN CDXZ_HUMAN ALEU_HORVU AAT_STRVG HISX_METTH	PRT; 11 ted) sequence upc annotation u n PC 7210. ta; Craniata; ia; Sciurogne ia; Sciurogne 100 E., Schil Loh E., Schil Loh E., Schil	FRAMEWORK-1. COMPLEMENTARI FRAMEWORK-2. COMPLEMENTARI COMPLEMENTARI COMPLEMENTARI FRAMEWORK-3. ET SIMILARITY BY SIMILARITY 69F1A5CE886	Score 31; DB Pred. No. 0.8 ; Mismatches	D; PRT; 1. Created) Last sequence up. Last annotation region CBPC 101. nordata; Craniata
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                                         MEDITINE=79012520; PubMed=99744;
McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                      related mouse Kappa variable regions.";

Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).

1- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

PIR. A01936; KVMSCI.

HSSP; P80362; IWTL.

InterPro; IPR003006; Ig_MHC.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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COMPLEMENTARITY - DETERMINING - 3.
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 7043.
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HSSP; P80362; 1MTL.
InterPro; IPR003506; Ig_MC.
InterPro; IPR003596; Ig_V.
Ffan; PF00047; Ig; 1.
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Immunoglobulin V region.
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Mammalia; Eutheria; Rodentía; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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MEDLINE=79073152: PubMed=103003;
Weigert M., Gatmaltan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=79073152; PubMed=103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Appa chain V-III region PC 7769.
Mus musculus (Mouse).
                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 7183.
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Nature 276:785-790(1978).
PIR; B01937; KWMS83.
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InterPro; IPR003006; Ig_MHC.
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
                                       Conservative
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 Query Match
Best Local Similarity
Matches 7; Conserv
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Matches 7; Conserv
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ID KV3N_MOUSE
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KV3Q_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAINER KW20, ATCC 51907;

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-!- SIMILARITY: STRONG, TO E.COLI YIEO.
-!- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB 1; Length 111; pred. No. 0.87; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                         COMPLEMENTARITY - DETERMINING-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6FAA345279356829 CRC64;
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15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical transport protein H10852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 AA.
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diversity.";
Nature 276:785-790(1978).
PIR; E01937; KVMS69.
HSSP; P80362; IWTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Query Match
Best Local Similarity 10vo..
"Loc 7; Conservative
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SMART; SM00406; IGV; 1.
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Laure C.J., Watanabe S., Hilschmann N.;
"The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin dal.), I. The amino acid sequence of the L-chain of kappa-type, subgroup I.";
hoppe-seyler's Z. Physiol. Chem. 354:1503-1504(1973).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
TIGR; H10852; -.
InterPro; IPR004638; Efflux_EmrB.
InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
TIGRFAMS; TIGR0711; efflux_EmrB; 1.
Hypothetical protein; Transport; Transmembrane; Inner membrane;
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COMPLEMENTARITY-DETERMINING-1.
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D725EFFD50F9F23F CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-I region GAL.
Homo sapiens (Human).
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HSSP, P01607; IREI.
InterPro; IPR001306; Ig_MHC.
Interpro; IPR001356; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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Matches 7; Conservative
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463 AA;
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108 AA;
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P01599:
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                                       Gaps
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-!- SIMILARITY: TO RICE DWARF VIRUS S9 AND RICE GALL DWARF VIRUS S10.
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89263810; PubMed=2726499;
Dall D.J., Anzola J.V., Xu Z., Nuss D.L.;
"Complete nucleotide sequence of wound tumor virus genomic segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillman B.I., Anzola J.V., Halpern B.T., Cavileer T.D., Nuss D.L.; "First field isolation of wound tumor virus from a plant host: minimal sequence divergence from the type strain isolated from an
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                                                                                                                                                                                                                             01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
Structural protein P9 (Capsomere protein P9) (Protein PNS11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VP9_WTVNJ STANDARD; PRT; 313 AA.
P31611;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
Structural protein P9 (Capsomere protein P9) (Protein PNS11).
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 DB 1; Length 108;
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                                                                                                                                                                                                                                                                                                                                      Viruses; dsRNA viruses; Reoviridae; Phytoreovirus.
NCBL_TaxID=10987;
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Viruses; dsRNA viruses; Reoviridae; Phytoreovirus.
NCBI_TaxID=31595;
                                                                                                                                                                                                 313 AA.
                    . 4.8;
90.3%; Score 28; DB
85.7%; Pred. No. 4.8;
ive 1; Mismatches
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MEDLINE=92074261; Pubmed=1962460;
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                                     6; Conservative
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294 AASNLDS 300
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50 AASNLQS 56
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 Query Match
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P12326;
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                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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between the Swiss Institute of Bioinformatics and the EMBL outstation
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Cell division; AFP-binding; Transmembrane; Hydrolase; Metalloprotease;
Zinc; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99120557; PubMed-9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Moonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Urida-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
-!- FUNCTION: SEEMS TO ACT AS AN ATP-DEPENDENT ZINC METALLOPEPTIDASE
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori 199 (Campylobacter pylori 199).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                    Score 28; DB 1; Length 313; Pred. No. 15;
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                   Nonstructural protein.
SEQUENCE 313 AA; 35551 MW; D9B904785C601C34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- COFACTOR: BINDS 1 ZINC ION (POTENTIAL).
-:- SUBCELLULAR LOCATION: INTEGRAL Membrane protein.
-:- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY 2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-JUN-2002 (Rel. 41, Last annotation update)
Cell division protein ftsH homolog (EC 3.4.24.-).
FTSH OR JHP00356
                                                                                                                                                                                                                                                                                                                                                                                                                                                   632 AA.
                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE001471; AAD05932.1; -.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003959; AAA_ATPase_centr.
InterPro; IPR003960; AAA_Sub.
InterPro; IPR000642; Peptidase_M41.
Pfam; PF00004; AAA; 1.
Pfam; PF01434; Peptidase_M41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00382; AAA; 1.
TIGRFAMS; TIGR01241; FtsH_fam; 1.
                                                                                                                                                                                                                                 90.3%;
85.7%;
                                                                                                                                   EMBL; M77020; AAA48500.1; -.
                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                       PIR; C41705; QMXRWN.
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                    1 AASNLES 7
                                                                                                                                                                                                                                                                                                                                                                                                                                             FTSH_HELPJ
Q9ZM66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trust T.J.;
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                                                                                                                                                                                                                                                                          Matches
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RA Admins M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D., Admanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Genorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Evator G.G., Mortman J.R., Andell M.D., Zhang Q., Chen L.X., Button G.G., Wortman J.R., Andrews-Pfannkoch C., Baldwin D., RA Mani M.H., Doyle C., Baxter E.G., Helt G., Melson C.R., Miklos G.L.G., Ratil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ra Ballew R.M., Basu A., Berman B.P., Brandari D., Bolshakov S., Benos P.V., Berman B.P., Brandari D., Bolshakov S., Buttis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., Rabeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P., Ra de Pablos B., Delcher A., Deng Z., Mays A.D., Dew II., Diaties P., Buttis K.C., Busam D.A., Butler H., Cadleu E., Canter A., Chandra I., Rablosh E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Bourbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Glodek A., Gong F., Garrell J.H., Gu Z., Guan P., Harris M.L., Harvey D., Helman T.J., Harris M.L., Ibegwam C., Alalali M., Kalush F., Karlush F., Karlon G.H., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Matterla B., Mourt S.M., Moy M., Murphy B., Murphy L., Mozins J., Moshrefi A., Mourt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Puri V., Resee M.G., Rablazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Schen H., Rahent F., Sanner R.A., Shue B.C., Scheeler F., Shen H., Rahener K., Seniert K., Seniert K., Seniert K., Seniert K., Shues E., Shan H., Shimson J.K., Shueseler F., Shen H., Shimson J.K., Shueseler F., Shen H., Shimes B.C., Siden-Kamos I., Simpson M., Skupski M.P., Shilth T.,
                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kinesin-11ke protein Kip6BD.

Kip6BD OR Kip5 OR CG7293.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophiliae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pesavento P.A., Stewart R.J., Goldstein L.S.B.,; "Characterization of the KLP68D kinesin-like protein in Drosophila: possible roles in axonal transport."; J. Cell Biol. 127:1041-1048(1994).
                                                                                                                                                                                                                                      ;
                                                                         ATP (POTENTIÀL).
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                      (CATALYTIC) (BY SIMILARITY)
                                                                                                                                                                                                DB 1; Length 632;
                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                         2FB67B43C51559FB CRC64;
                    PERIPLASMIC (POTENTIAL).
                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                  P46867; Q9VTN8;
01-NOV-1995 (Rel. 32, Created)
10-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                  BY SIMILARITY.
ZINC (CATALYTI
                                                                                                                                                                                                              Pred. No. 33;
1: Mismatches
                                          POTENTIAL.
                                                                                                                                                                                                  Score 28;
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Berkeley;
MEDLINE-20196006; PubMed=10731132;
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MEDLINE=95050960; PubMed=7525600;
                                                                                                                                                         69765 MW;
                                                                                                                                                                                                90.3%;
                                                                                                                                                                         Ouery Match
Best Local Similarity 85...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                              434
435
438
632 AA;
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616 AANNLES 622
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ID KL68_DROME
                  DOMAIN
TRANSMEM
                                                                                                                  ACT_SITE
METAL
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  TRANSMEM
                                                         DOMAIN
NP_BIND
                                                                                                  METAL
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                  kinesin superfamily in Drosophila.";
Proc. Natl. Acad. Sci. U.S.A. 88:8470-8474(1991).
-! FUNCTION: PLUS-END DIRECTED MICROTUBULE MOTOR THAT MAY BE USED FOR ANTEROGRADE AXONAL TRANSPORT AND COULD CONCEIVABLY MOVE CARGOES IN FLY NEURONS DIFFERENT THAN THOSE MOVED BY KINESIN HEAVY CHAIN OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN II SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THE CENTRAL NERVOUS SYSTEM AND IN A SUBSET OF THE PERIPHERAL NERVOUS SYSTEM DURING
                                                                                                                                                                                                                                 Stewart R.J., Pesavento P.A., Woerpel D.N., Goldstein L.S.B.; "Identification and partial characterization of six members of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 784;
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GSRAK -> VRGQV (IN REF. 3).
G -> A (IN REF. 2).
94BB9BADF072DFC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00129; KISc; 1.
PROSITE; PS00411; KINESIN MOTOR_DOMAIN1; 1.
PROSITE; PS0067; KINESIN MOTOR_DOMAIN2; 1.
MOTOR PROFILE; PS0067; KINESIN MOTOR_DOMAIN2; 1.
MOTOR PROFILE; PS0067; MICROTUBDIES; ATP-binding; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Appa chain V-I region AU.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KINESIN-MOTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; 198001752; kinesin_motor. Pfam; PF00225; kinesin; 1. PRINTS; PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                  OTHER PLUS-END DIRECTED MOTORS.
                                                                                                                                                                                         SEQUENCE OF 220-342 FROM N.A. MEDLINE=92020874; PubMed=1924306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE003543; AAF50008.1; -. HSSP; P17119; 3KAR. FlyBase; FBgn0004381; Klp68D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88193 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U15974; AAA69929.1; -. EMBL; M74431; AAA28658.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.3%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          784 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBRYOGENESIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KV1B_HUMAN
P01594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
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0
                                                                                                                                                                                                                                                              Bence-Jones protein Au.";
Biophys. Struct. Mech. 1:139-146(1975).
-!- MISCELLEAMBOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF THE KAPPA CHAIN REI.
                                                                                                                                                                                                                                                                                                                                        -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                        Schiechl H., Hilschmann N.; "Rule of antibody structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                 MEDLINE-77022433; PubMed=1234024;
Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
Schwager P., Steigemann W., Schramm H.J.;
"The structure determination of the variable portion of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY - DETERMINING - 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.1%; Score 27; DB 1; Length 108; 100.0%; Pred. No. 8.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E8011187EE6F6FB9 CRC64;
                                                                                                                                                    Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::
                                                                                                                                                                                                                                                                                                                                                                       PIR; A01862; KIHUAU.
HSSP; P01607; IREI.
INCEPERO; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_V.
Pfam; PR00047; Ig; Il_C.
Immunoglobulin V region; Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. No. 8.5 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMEWORK-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                          MEDLINE=72189444; PubMed=5028201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
MEDLINE=79073152; PubMed=103003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11939 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P80362; 1WTL.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 276:785-790(1978).
PIR; A01940; KVMS54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49
56
88
97
107
88
                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY
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57
89
98
23
108
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nes 6; Conserv
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                             NCBI_TaxID=9606;
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51 ASNLES 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ASNLES 7
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P01674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
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                                                           SEQUENCE
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MEDLINE=79012520; PubMed=99744;
MCKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).

-! MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
PIR; A01934; KVMS37.
HSSP; P01679; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Ffam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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COMPLEMENTARITY-DETERMINING-2.
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                                                                                                   COMPLEMENTARITY - DETERMINING - 3.
                                                                                                                                                                  87.1%; Score 27; DB 1; Length 108; 100.0%; Pred. No. 8.5; o; Indels ive 0; Mismatches 0; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1996 (Rel. 38, Last annotation update)
19 Kappa chain V-III region PC 3741/TEPC 111.
                                                                                                                         BY SIMILARITY.
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BY SIMILARITY.
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MEDLINE=79073152; PubMed=103003;
InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 276:785-790(1978).
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MEDLINE=79012520; PubMed=99744;
MCKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions."; 175:3913-3917(1978).
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P01662.
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region ABPC 22/PC 9245.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBL_TAXID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                             diversity.";

Nature 276:785-790(1978).

-!- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.

PIR; A01935; KVMSMG.

HISSP: P01679; 2FBJ.

Interpro; IPR003506; Ig_MC.

Interpro; IPR003566; Ig_V.

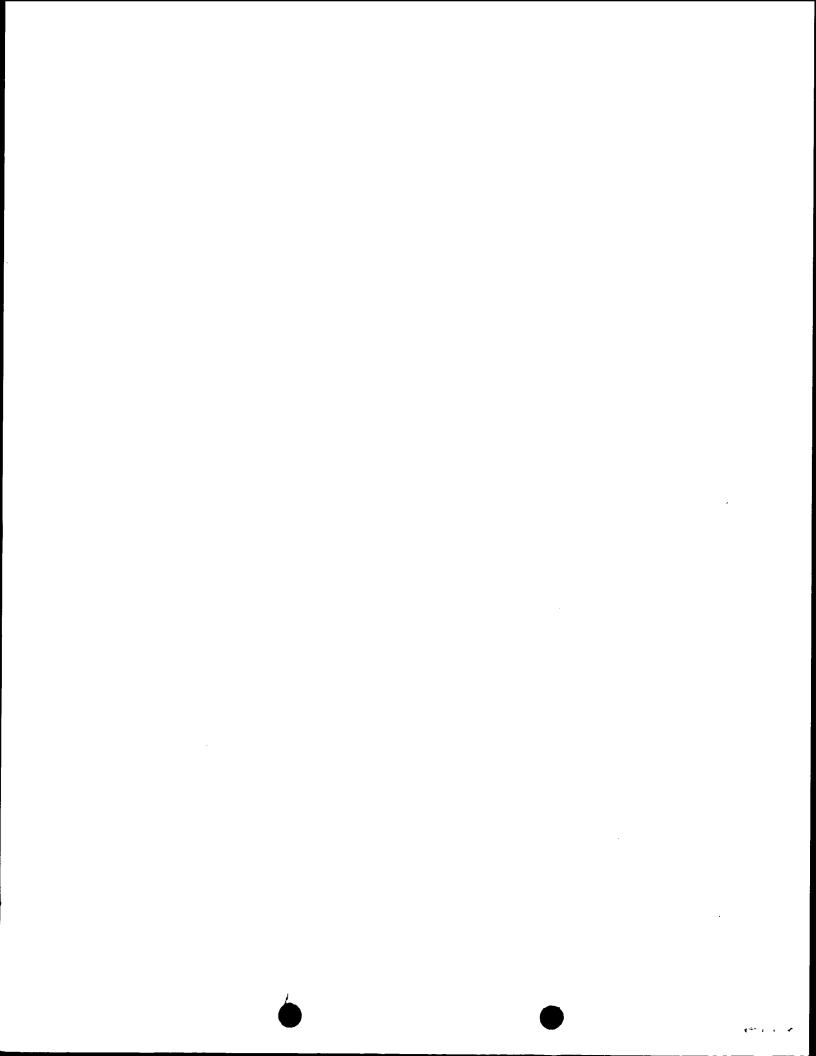
Pfam; PF00047; ig; 1.

SMART; SM00406; IGV; 1.

Immunoglobulin V region.

FRAMEWORK-1.
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SEQUENCE (PC 9245).
MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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Search completed: February 14, 2003, 11:16:23 Job time: 4.6129 secs



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February 14, 2003, 11:10:17; Search time 14.5645 Seconds (without alignments) 99.030 Million cell updates/sec
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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SUMMARIES

	Description	Q96rs9 homo sapien	042938 schizosacch	075162 homo sapien	Q8yf10 brucella me	Q9j180 mus musculu	Q9u2y4 caenorhabdi	Q9a698 caulobacter	Q8u760 agrobacteri	Q9atd5 gossypium h	Q8ysw1 anabaena sp	Q961h5 drosophila	Q920e9 mus musculu	P94981 mycobacteri	Q8yef7 brucella me	Q9saf7 arabidopsis	Q9m887 arabidopsis
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Q9L176 Q9LEX3 Q9ASW0 Q9LEX3 Q9LEX3 Q9LEX3 Q9C128 Q9C128 Q9LSX2 Q9F9H4 Q9LSX2 Q9PHD5 Q9PHD5 Q9PHD5 Q9PHD5 Q9PHD5 Q9PHD5 Q9PHD5 Q9PHD5 Q9PHD5 Q9PHD6 Q9PHD6 Q9PHD7 Q9	ALIGNMENTS PRT; 508 AA Created; Last sequence u Last annotation ; Craniata; Ver ; Catarrhini; H ts with DAZ Pro EMBL/GenBank/DD ; EF2C079B11A1 Score 31; DB Pred. No. 24; 0; Mismatches	PRT; 942 AA 06, Created) 06, Last sequence u 21, Last annotation kinase beta subunit (Phosphohexokinase)
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                                                                           Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M.; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + D-FRUCTOSE 6-PHOSPHATE = ADP + D-FRUCTOSE 1,6-BISPHOSPHATE = ADP + D-FRUCTOSE 1,6-BISPHOSPHATE STEP OF GLXCOLYSIS.
-!- PATHWAY: KEY CONTROL STEP OF GLXCOLYSIS.
-!- SUBUNIT: HETEROCTAMER OF 4 ALPHA AND 4 BETA CHAINS (BY
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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               Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
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Last annotation update)
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         Schizosaccharomyces pombe (Fission yeast).
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Matches 7; Conservative
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                                  Schizosaccharomyces.
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DelVecchio V.G., Kaparal V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Salkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.; The genome sequence of the facultative intracellular pathogen Broc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

EMBL; Ac009587; AAL52691.1; -. EMBL; Ac00359; Cold_shock.

Prom. PROMOSO; ColdShock.

PRINTS; PROMOSO; ColdShock.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus muscuíus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 28; DB 16; Length 69; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-001-2000 (TrEMBLrel. 15, Created)
01-001-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 AA; 7301 MW; D6142414631FDEBA CRC64;
                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                     STRAIN-16M / ATCC 23456 / BIOTYPE 1;
MEDLINE-20020109; Pubmed-11756688;
                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with cardiac myosin.";
Infect. Immun. 68:5803-5808(2000).
EMBL. AF206026; AAF69324.1;
INSPP. P80362; JUVIL.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/C;
MEDLINE=20448942; PubMed=10992488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00357; CSP; 1.

SMOSITE; PS00352; COLD_SHOCK; 1.

Complete proteome.

SEQUENCE 69 AA; 7301 MW; D614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.3%;
85.7%;
                                     01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
  PRELIMINARY;
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                                                                                                    Cold shock protein CSPA.
                                                                                                                                                                                      Brucellaceae; Brucella.
NCBI_TaxID=29459;
                                                                                                                                               Brucella melitensis.
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Best Local Similarity
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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| 62 AAANLES 68
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Q8YFL0
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156 AASNLET 162
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Q8U760
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STRAIN=ATC. 19089 / CB15;
MEDLINE=21173698; PubMed=11259647;
Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Nierman W.C., Feldblyum T.V., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                  Gaps
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Caulobacter.
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0
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0
                                                                           90.3%; Score 28; DB 11; Length 103; 85.7%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.3%; Score 28; DB 5; Length 204; 85.7%; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                       'Genome seguence of the nematode C.elegans: A platform for
                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                  investigating biology.";
Science 282:2012-2018(1998).
EMBL; AL132858; CRB60484.1; -
SEQUENCE 204 AA; 23067 MW; 8968065DF2EA9C7E CRC64;
                                                         11224 MW; EC87D653DB3AAB21 CRC64;
                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein CC2196.
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                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16,
InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 1. SMART: SMO0406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 85.7
Matches 6; Conservative
                                                                            Query Match 90.3'
Best Local Similarity 85.7'
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caulobacter crescentus
                                                103
                                     NON_TER 103 SEQUENCE 103 AA;
                                                                                                                                                                                                                                             Y113G7A.14 protein.
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134 SASNLES 140
                                                                                                                                 1 AASNLES 7
                                                                                                                     1 AASNLES 7
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Q9A698
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Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21668550; PubMed=11743193; Monks D.E., Kitajima J.P., wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chen Y., Paulsen I.T., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nester E.W.; "The genome of the natural genetic engineer Agrobacterium tumefaciens CSR":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21608551; PubMed=11743194; Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Gielome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Rhizobiaceae; Rhizobium.
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                                                                                                                                                                                                                                                                                                                                    Score 28; DB 16; Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                   Hypothetical protein; Complete proteome.
SEQUENCE 209 AA; 22181 MW; D0200247FF7E9E2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein Atu4594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agrobacterium tumefaciens (strain C58 / ATCC 33970)
                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 294:2323-2328(2001).
EMBL; AE009387; AAL45388.1; -.
EMBL; AE008228; AAK88851.1; -.
                                                                                                                                                                     EMBL; AE005891; AAK24167.1; -.
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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Best Local Similarity
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Best Local Similarity
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6; Conservative
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Best Local Similarity
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                                                                                                                                                                KLP68D OR CG7293.
                         378 AASNLDS 384
                                                                                                                                                                                                                                                               STRAIN=BERKELEY;
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 1 AASNLES
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                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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Hypothetical protein: Complete proteome.
SEQUENCE 579 AA; 66557 MW; 5C00EBDBCF31BB97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 16; Length 57
Pred. No. 1.6e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                  Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SINILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL; AF336282; AAK19615.1; -.
HSSP; P06876; 1MBK.
                                                                                                                                                                                                                                                                                              InterPro; JPR001005; Myb_DNA_binding.
Pfam; PF00249; myb_DNA-binding; 2.
SMART; SM00395; SANT; 2.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
PROSITE; PS00037; MYB_2; 1.
PROSITE; PS00090; MYB_2; 1.
DNA-binding; Nuclear protein.
SEQUENCE 302 AA; 33816 MW; 48EE5D9D921ED2D7 CRC64;
                                               (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 20, Last sequence update) (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=ACALA MAXXA; TISSUE=DAY OF ANTHESIS OVULE;
MATZ E.C., Burr B.;
"Cotton seed fibers are trichomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    579 AA
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01-MAR-2002 (TrEMBLrel. 20, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last anno
                                                                                                               Gossypium hirsutum (Upland cotton).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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MEDLINE-21595285; PubMed-11759840;
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                         PRELIMINARY;
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Best Local Similarity
6; Conserv
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286 AASNLQS 292
                                                                                                                                                              NCBI_TaxID=3635;
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                                                              01-JUN-2001
01-MAR-2002
                                                 01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QBYSW1;
                                                                                                  GHMYB10
                         Q9ATD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8YSW1
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Q8YSW1
ID Q8YSWI
RESULT 9
Q9ATD5
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SEQUENCE
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                   Gaps
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole genome comparison of Mycobacterium tuberculosis clinical and labbratory strains.";
Submitted (ASR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; 285982; CAB06640.1; -.
EMBL; AE007031; AAK45953.1; -.
                                                                                                                                                                                          Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                    ;
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87.1%; Score 27; DB 11; Length 111;
100.0%; Pred. No. 48;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.1%; Score 27; DB 16; Length 31
85.7%; Pred. No. 1.5e+02;
"..ma+rhes 1; Indels
                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Complete proteome.
30219 MW; F51DFE4CC2D9EDAD CRC64;
                                                                                                                       01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 30.2 kDa protein (PE family protein).
RV1646 OR MTCY06HII.11 OR MT1684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
                                                                                                       310 AA.
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                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuberculist; Rv1646; -.
InterPro; IPR000084; PE_region.
Pfam; PF00934; PE; I.
ProDom; PD001223; PE_region; I.
Hypotheting protein; Complete p
SEQUENCE 310 AA; 30219 MW; F
                                                                                                                                                                        Mycobacterium tuberculosis.
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 Query Match 87.1
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                   NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AASNLES 7
                                                         55 ASNLES 60
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                                      2 ASNLES 7
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                                                                                                                P94981;
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                                                                                     RESULT 13
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SEQUENCE FROM N.A.
STRAIN-[6M / ARCC 22456 / BIOTYPE 1;
MEDLINE-20020109; PubMed=11756688;
MEDLINE-20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
Fre genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CV. COLUMBIA;
Vysotskala V.S., Schwartz J.R., Yu G., Toriumi M., Lee J.M., Lenz C.,
Liu S., Li J., Kremenetskala I., Luros J., Ngan I., Genzalez A.,
Altafi H., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P.,
Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P.,
Bavis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
Arabidopsis thaliana chromosome I BAC F3F19 sequence.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC007357; AAD31076.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSTIE; PSO0572; GLYCOSYL_HYDROL_FI_1; UNKNOWN_1.
SEQUENCE 389 AA; 43216 MW; 1DC342A0BF4B7EBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36286 MW; 2092FC153E63A80C CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
F3F19.26 protein.
01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Acetoacetyl-CoA synthetase (EC 6.2.1.16).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.1%; Score 27; DB 16; 1
100.0%; Pred. No. 1.6e+02;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003592; LRR_out.
Pfam; PF00560; LRR; 8.
PRINTS; PR00019; LEURICHRPT.
SMART; SM00370; LRR; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001360; GH_1.
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ligase; Complete proteome.
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                                                                                               Brucella melitensis.
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                                                                                                                                                                                               NCBI_TaxID=29459;
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25 AASNLE 30
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0;
Query Match 87.1%; Score 27; DB 10; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps
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2 ASNLES 7 |||||| 106 ASNLES 111

Dp

Search completed: February 14, 2003, 11:18:43 Job time : 16.7312 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 14, 2003, 11:04:17; Search time 24.3871 Seconds Run on:

(without alignments)
49.176 Million cell updates/sec

US-09-701-001B-6 1 QQSSEDPPT 9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 ched:

Scoring table:

908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

908470

Database

A_Geneseq_101002:*

Maximum Match 100% Listing first 45 summaries

Post-processing: Minimum Match 0%

/SIDS2/gcgdata/geneseg/genesegp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA2002.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:* /SIDS2/gcgdata/geneseg/geneseqp-embl/AA1983.DAT:*/SIDS2/gcgdata/geneseg/geneseqp-embl/AA1984.DAT:*/SIDS2/gcgdata/geneseg/geneseqp-embl/AA1985.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Antibody 4H5 L cha	Murine CD4/CD34 re	Antibody 4H5 L cha	Murine derived pro	Antibody 4H5 L cha	Murine derived pro	Murine derived pro	Anti-CD4 antibody	Antibody 4H5 H cha	Antibody 4H5 L cha
	ID		AAY51138	AAY59263	AAY51140	AAY59267	AAY51144	AAY51146	AAR32123	AAY 59264	AAY59265
	DB	21	21	21	21	21	21	21	14	21	21
	Length	6	6	103	103	111	111	111	131	305	305
dР	Query e Match Length DB I	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	48	48	48	48	48	48	48	48	48	48
	Result No.		2	3	4	Ŋ	9	7	ω	σ	10

Murine derived pro Murine derived pro MAD 3B9 light chai CDR of the light c Light chain CDR fo Light chain variab	Light chain sequen p64 44 protein pro Humanized antibody Light chain of Hum Light chain of Mum Light chain of Mum Light chain of Mum	chain MAb 3B chain chain	Anti-Leu 3a 11ght Anti-Leu 3a 11ght Humanized antibody CDR of the light c Light chain CDR fo Mouse Kappa III 1i Humanized antibody Light chain variab	Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia A. thaliana transc Arabidopsis transc Arabidopsis thalia Monoclonal antibod Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia
AAY5114 AAY5114 AAR7019 AAY2377 AAY1811	AAY181 AAR290 AAR702 AAW302 AAW302	AAY181 AAR701 AAY237 AAY181 AAR661		AAY181 AAG414 AAG414 AAU929 AAG414 AAG299 AAG299
05 2 05 2 9 1 9 2 2 11 2 2	331 12 23 33 1 1 2 3 3 1 1 2 3 3 1 1 2 3 3 1 2 3 3 1 2 3 3 1 2 3 3 1 3 3 3 1 3 3 3 1 3	132211	31 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	31 20 82 21 001 21 004 22 004 23 118 21 115 16 95 21 17 21
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11 12 13 14 15	17 18 19 20 21	2222 2524 2654	2 2 3 3 3 3 5 6 8 8 8 9 9 8 8 9 9 9 8 9 9 9 9 9 9 9 9	38 337 338 338 344 444 344 344 344 344 344

ALIGNMENTS

Antibody 4H5 L chain variable region CDR3 fragment. CD4 antigen; anti-human; antibody; 4H5; drug; CDR; complementarity determining region. AAY59261 standard; peptide; 9 AA (ASAH) ASAHI KASEI KOGYO KK 98JP-0163034, 98JP-0163034 (first entry) JP11332563-A. 26-MAY-1998; 26-MAY-1998; 17-APR-2000 07-DEC-1999 AAY59261; Mus sp. RESULT 1 AAY59261

An antibody and the nucleic acid coding the antibody WPI; 2000-091351/08.

Claim 2; Page 14; 25pp; Japanese

The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoletic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of the production and autoimmune diseases. This sequence represents a murine derived complementarity determining the composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells \,
                   (CDR)-1,
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application for drugs. It is highly safe in human dose. Sequences AAY59259-61 represent the complementarity determining region (CDR:CDR-2 and CDR-3 fragments in the L chain variable region of the
                                                                                                                                                                                                                                                                                                                                                                                                                      Murine CD4/CD34 recognizing antibody light chain CDR-3 region #1.
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                                                                                                                       100.0%; Score 48; DB 21;
100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
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100.0%; Score 48; DB 21;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soka T, Morimoto I, Miyamura K;
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                                                                                                                                                                                                                                                                                                                  AAY51138 standard; Protein; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ASAH ) ASAHI KASEI KOGYO KK.
(ASAH ) ASAHI MEDICAL CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-JP02711.
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98JP-0163023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDR-3; light chain; murine.
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                   antibody 4H5 respectively
                                                                                                                                         Best_Local Similarity 100.
Matches 9; Conservative
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26-MAY-1998;
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AAY51138
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1 QOSSEDPPT 9

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Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                                              The invention provides an antibody having affinity to CD4 antigen. Th anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the L chain variable region of the antibody 4H5.
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                                                                                                                                                          CD4 antigen; anti-human; antibody; 4H5; drug.
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                                                                                                                                   Antibody 4H5 L chain variable region.
                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 15-16; 25pp; Japanese.
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                                                                AAY59263 standard; protein; 103 AA.
                                                                                                                                                                                                                                                                                              (ASAH ) ASAHI KASEI KOGYO KK.
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Best Local Similarity
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QOSSEDPPT
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Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
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                                         21; Length 111;
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                                        100.0%; Score 48; DB 21 100.0%; Pred. No. 0.64;
                                                                    Mismatches
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                                                                                                                                                                                                            AAY51144 standard; Protein; 111 AA.
                                                                                                                                                                                                                                                                                                    Murine derived protein fragment #6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ASAH ) ASAHI KASEI KOGYO KK
(ASAH ) ASAHI MEDICAL CO LTD
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Matches 9; Conserv
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nes 9; Conserv
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            111 AA;
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26-MAY-1998;
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                                                                                                                                                                Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells
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                                                                                         Soka T, Morimoto I, Miyamura K;
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                                            (ASAH ) ASAHI KASEI KOGYO KK.
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98JP-0159957.
98JP-0163023.
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Best Local Similarity 100.
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N-PSDB; AAZ44204.
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25-MAY-1998;
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   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of Lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                      Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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T-helper cell inhibition; transplant rejection; MAb;
interleukin-2 receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 48; DB 21; Length 111; 100.0%; Pred. No. 0.64;
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                                                                                                                                                                                                                                                                     Soka T, Morimoto I, Miyamura K;
                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 97-98; 111pp; Japanese.
AAY51146 standard; Protein; 111 AA.
                                                            Murine derived protein fragment #8.
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(ASAH ) ASAHI MEDICAL CO LTD.
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                                       31-MAR-2000 (first entry)
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est Local Similarity
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                                                                                                                                             WO9961629-A1
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This sequence is the light chain variable region of a preferred anti-CD4 monoclonal antibody for use in the claimed synergistic composition. MAD MT 3.10 is deposited as clone 3.101/sB10 (ECACC 90090702). The anti-CD4 antibody is used with at least one anti-ILZR alpha or beta antibody. Individually the antibodies are strongly inhibiting and when used together their immunosuppressive properties are improved; they synergistically inhibit T-helper cell proliferation to effectively inhibit transplant rejection at low access without significantly reducing the general immune response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha- or anti-IL2R beta antibodies
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/label= signal
21.120
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121..131
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Sequence

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AAY59265;

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Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Devices containing antibodies recognising CD4 or CD34 and their use for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 48; DB 21; Length 305; 100.0%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the separation of CD4 or CD34 positive cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miyamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 22; Page 80-82; 111pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY51142 standard; Protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine derived protein fragment #4.
                   AAY51141 standard; Protein; 305 AA.
                                                                                                                               Murine derived protein fragment #3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             KASEI KOGYO KK
MEDICAL CO LTD
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98JP-0163023.
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 QQSSEDPPT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ44205
                                                                                                                                                                                                                                                                                                                                                                                                                                             (ASAH ) ASAHI
(ASAH ) ASAHI
                                                                                                                                                                                                                                                                           WO9961629-A1.
                                                                                                                                                                                                                                                                                                                                                   24-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-1998;
                                                                                          31-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY51142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                           Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ono M,
   AAY51141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
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                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                              The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the H chain sequence of the antibody 4H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the L chain sequence of the antibody 4H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
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                                                                                                                                                                                                                                                                                             100.0%; Score 48; DB 21; Length 305; 100.0%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 48; DB 21; Length 305; 100.0%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                          An antibody and the nucleic acid coding the antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD4 antigen; anti-human; antibody; 4H5; drug.
                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                           Disclosure; Page 16-17; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY59265 standard; protein; 305 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody 4H5 L chain sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ASAH ) ASAHI KASEI KOGYO KK
(ASAH ) ASAHI KASEI KOGYO KK
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                                      WPI; 2000-091351/08
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es 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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248 QQSSEDPPT 256
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                                                                                                                                                                                                                                                          305 AA;
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                                                     N-PSDB; AAZ58663
                                                                                                                                                                                                                                                                                                                                                                      1 QQSSEDPPT
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Gaps

0;

Indels

Sequence

RESULT 11

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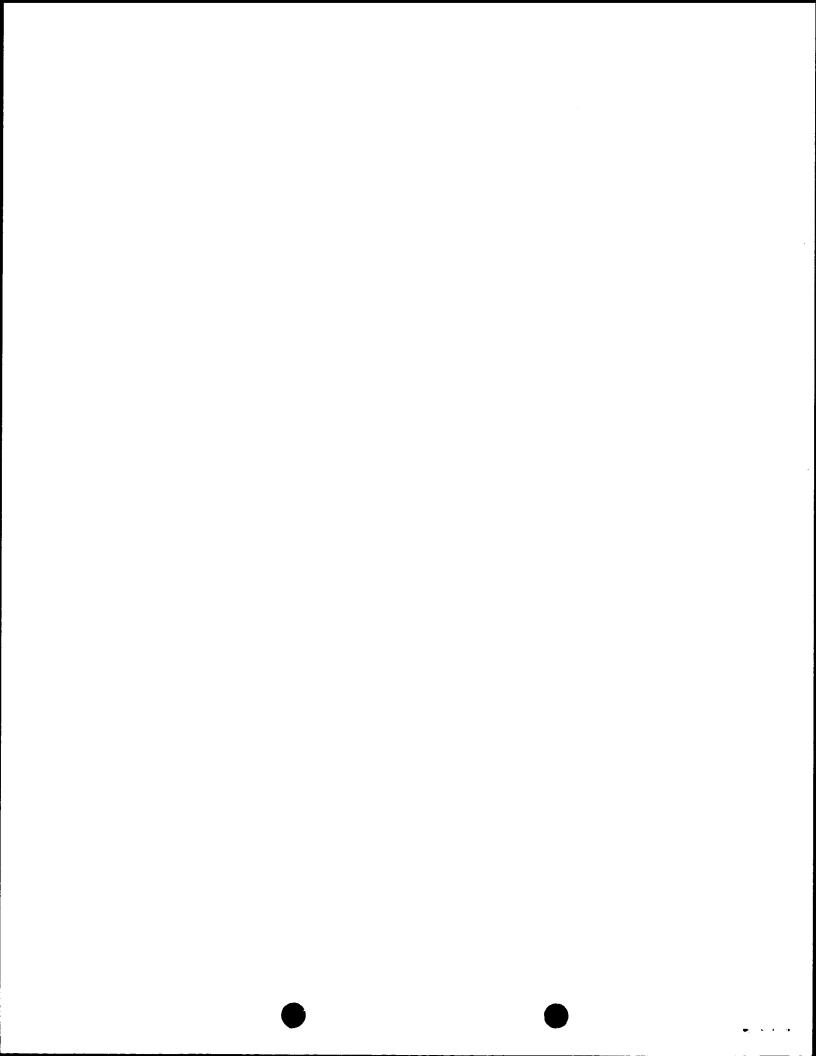
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07-SEP-1993;
14-OCT-1993;
07-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                            13-SEP-1999
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                                                                                                                                                            identified
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       Gross MS,
                                                                                                                                                                                                                                                                                                                         AAY23774;
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                           This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HTV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used
                                                                                                                                                                                Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 21; Length 305; Pred. No. 1.7; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric antibody; humanized antibody; antibody engineering; monoclonal antibody; MAb; interleukin-4; IL-4; allergy; CDR; complementarity determining region.
                                                                                                                                                                                                                                                                                                                  to illustrate the method of the invention.
                                                                                                                                  Soka T, Morimoto I, Miyamura K;
                                                                                                                                                                                                            Claim 22; Page 82-84; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR70197 standard; Protein; 9 AA
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0
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100.0%;
                                                                                                      (ASAH ) ASAHI KASEI KOGYO KK
(ASAH ) ASAHI MEDICAL CO LTD
                                                       99WO-JP02711
                                                                          98JP-0159957.
98JP-0163023.
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93US-0136783
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAb 3B9 light chain CDR
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
9; Conserve
                                                                                                                                                  WPI; 2000-086720/07.
                                                                                                                                                                                                                                                                                                                                                                                                      11111111
248 QQSSEDPPT 256
                                                                                                                                                                                                                                                                                                                                    305 AA;
                                                                                                                                                                                                                                                                                                                                                                                           1 QQSSEDPPT 9
                                                                                                                                                              N-PSDB; AAZ44206
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14-OCT-1993;
                  WO9961629-A1
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                                                       24-MAY-1999;
                                                                         25-MAY-1998;
26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9507301-A.
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                                     02-DEC-1999
                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR70197;
                                                                                                                                  Ono M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus sp.
Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR70197
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Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy; complementarity determining region.
                                                                                                                                                                                                                                                                                                  Spleen cells from mice immunized with human IL-4 were used to prepare hybridomas, which were screened for anti-IL-4 MAD secretion. Only clone 3B9 was positive. cDNA clones of the 3B9 light and heavy chains were cloned into pGEMT+ and transformed into E. coli DHS-alpha. A light chain cDNA clone was sequenced (AAQ83490) that encoded the protein given in AAR70189. 3 CDRS (AAR70195-97) were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                     Chimeric and humanised \rm IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of \rm IL-4-mediated and \rm IgE-mediated allergic conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.8%; Score 45; DB 16; Length 9; 88.9%; Pred. No. 7.8e+05; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDR of the light chain variable region of antibody 3B9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sylvester DR;
   Sylvester DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Column 45; 50pp; English.
                                                                                                                                                                                                                                                Disclosure; Page 56; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY23774 standard; Peptide; 9 AA.
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93US-0136783.
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Holmes SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-429500/36.
                                                               WPI; 1995-123387/16.
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nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAX85891.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease;
The present sequence represents a complementarity determining region (CDR) of the light chain variable region of murine interleukin-4 (ILL-4) antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans.
                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Light chain CDR for hIL-4 specific antibody.
                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complementarity determining region; CDR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Column 45; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY18116 standard; peptide; 9 AA.
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93US-0117366.
93US-0136783.
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88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gross MS, Holmes SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI: 1999-370482/31.
                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  1 QOSNEDPPT 9
                                                                                                                                                                                                                                                                                                                                                 1 QOSSEDPPT 9
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                                                                                                                                                                                                                                      9 AA;
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14-OCT-1993;
07-SEP-1994;
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                                                                                                                                                                                                                                        Sequence
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Gaps
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                                        Score 45; DB 20; Length 9; Pred. No. 7.8e+05; 1; Mismatches 0; Indels
                                                              1; Mismatches
                                                                                                                                      Search completed: February 14, 2003, 11:15:45 Job time: 24.3871 secs
                                        93.8%;
                                                                Conservative
versus host disease.
                                         Query Match
Best Local Similarity
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                     9 AA;
                                                                                   1 QOSSEDPPT
                                                                                               1 QQSNEDPPT
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                      Sequence
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Appl
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                                                         February 14, 2003, 11:13:07; Search time 8.12903 Seconds (without alignments) 32.575 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 73, Sequence 73, Sequence 33, Sequence 10, Sequence 10, Sequence 16, Sequence 58, Sequence 58,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4,
Sequence 11
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                                                                                                                                                                                                                                                                                               1: /cgg_Z_6/ptcdata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/laa/pcTuS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-483-632-20
US-08-483-632-73
US-08-137-1170-33
US-08-621-751A-10
US-08-621-751A-10
US-08-621-751A-10
US-08-483-636-2
US-08-483-636-2
US-08-483-632-2
US-08-483-632-2
US-08-483-632-2
US-08-483-632-14
                                                                                                                                                                                            al number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-461-379A-14
US-08-462-390B-14
                                                                                                                                                                          262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        - protein search, using sw model
                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                       Issued_Patents_AA:*
                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                US-09-701-001B-6
48
                                                                                                                      1 QOSSEDPPT 9
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Match Length
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Perfect score:
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29	34	9.0/	ע	า	PCT-US94-14105-43	sednence 43,	, Appl
c	34	70.8	106	٣	US-08-466-151-6	Seguence 6,	Appli
30	34	70.8	106	4	US-08-466-163B-6	Seguence 6,	Appli
31	34	70.8	111	_	US-08-491-845-8	Sequence 8,	Appli
32	34	70.8	111	-	US-08-491-845-16	Sequence 16,	, Appl
33	34	70.8	115	r	US-08-513-968-51	Sequence 51,	, Appl
34	34	70.8	131	4	US-08-579-378A-14	Sequence 14,	
35	34	70.8	131	4	US-08-579-378A-18	Sequence 18,	
36	34	70.8	218	2	PCT-US96-13152-2	Sequence 2,	Appli
37	33	68.8	28	'n	US-08-984-277-7	Sequence 7,	Appli
38	33	68.8	111	7	US-08-887-352B-5	Sequence 5,	Appli
39	33	68.8	111	7	US-08-887-352B-6	Sequence 6,	Appli
40	33	68.8	111	m	US-08-466-151-2	Sequence 2,	Appli
41	33	68.8	111	4	US-09-109-207C-5	Seguence 5,	Appli
42	33	68.8	111	4	US-09-109-207C-6	Sequence 6,	Appli
43	33	68.8	111	4	US-09-296-005-5	Sequence 5,	Appli
44	33	68.8	111	4	US-09-296-005-6	Sequence 6,	Appli
45	33	68.8	111	4	US-08-466-163B-2	Sequence 2,	App1i

ALIGNMENTS

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US-08-483-636-20

Sequence 20, Application US/08483636

Sequence 20, Application US/08483636

Sequence 20, Application US/08483636

SERERAL INCRAMINE Holmes, Stephen D. APPLICANY: Holmes, Stephen D. APPLICANY: Gross, Mitchell S. APPLICANY: Gross, Mitchell S. APPLICANY: Strucker Daniel R. I.4 Mediated Disorders OF SEQUENCES: 75

CORRESPONDENCE ADDRESS: 75

CONRESPONDENCE ADDRESS: ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P. O. Box 1539 / UW2220

CITY: King of Prussia ASTREE: PACKER STREET: P. O. Box 1539 / UW2220

CITY: King of Prussia COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM:
MEDIUM TYPE: PACHOLIN BATA: COMPUTER: PACHOLIN MARE: DATE OF STREET: US/08/483,636

FILING DATE: 07-SEP-1993

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: BRICK OF STREET: US/08/481,636

FILING DATE: 07-SEP-1994

APPLICATION NUMBER: PC-1994

APPLICATION NUMBER: PS-1994

APPLICATION NUMBER: PS-1993

FILING DATE: 07-SEP-1994

APPLICATION NUMBER: 18,00-509

FILING DATE: 07-SEP-1994

APPLICATION NUMBER: PS-1993

FILING DATE: 07-SEP-1994

APPLICATION NUMBER: PS-1994

APPLICATION NUMBER: PS-1994

APPRICATION NUMBER: PS-1994

APPLICATION NUMBER: PS
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MOLECULE TYPE: protein

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US-08-483-636-73
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Patent No. 5928904
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                          0; Indels
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                                      DB 2; Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: INC. COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/483,632
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
                                                     2e+05;
                                                                        1; Mismatches
                                      Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT/US/94/10308
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APPLICATION NUMBER: US 08/11/366
FILING DATE: 07-5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136/783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION NUMBER: CT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P50186-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                      93.8%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                          Conservative
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                 Query Match
Best Local Similarity
'Thag 8; Conserve
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Matches 8; Conserv
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1 QOSNEDPPT 9
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US-08-483-632-20
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 US-08-483-636-20
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Pred. No. 0.51;
1; Mismatches 0; Indels
                                                                            GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: STYVESTER, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKilne Beecham Corp./Corporate ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 73, Application US/08483632
Patent No. 592804
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY APPLICATION:
NAME: CANALT TECHNOLORY:
NAME: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOKNEY ABOUT Jeffrey A.
NAME: Sutton, Jeffrey A.
REGISTRATION UNDBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
Sequence 73, Application US/08483636 Patent No. 5914110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5024
INFORMATION FOR SEC ID NO: 73
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.8%;
88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 King of Prussia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-483-632-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οy
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RESULT 3

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ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
  OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 33, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEK: 904136
INFORMATION FOR SEQ ID NO: 33
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 131 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.97
است 8; Conservative
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
ADDRESSEE: SmithKline Beecham Corp./Corporate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 2;
Pred. No. 0.51;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                             FILING DATE:
PRIOR PEPERATION:
PRIOR APPLICATION OF THE APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY APPLICATION:
ANALY OF THE APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028 REFERENCE/DCKET NUMBER: P50186-3 TELECOMMUNICATION INFORMATION:
                      ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 33, Application US/08137117D Patent No. 5795965
GENERAL INFORMATION:
                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5020
INFORMATION FOR SEQ ID NO: 73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.8%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 93.8
Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 3000 K St
CITY: Washington
STATE: D.C.
                                                                                                         RY: USA
19406-0939
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US-08-137-117D-33
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Length 131;
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APPLICANT: SATO, KOh
APPLICANT: BENDIG, MARY
APPLICANT: BENDIG, MARY
APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 4.32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
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Pred. No. 0.6;
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGLEY HAROLD C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
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MONOCLONAL ANTIBODIES SPECIFIC FOR THE PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA RECEPTOR AND METHODS OF USE THEREOF
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                                                       Length 131;
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                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,751A
FILING DATE: 22-MAR-1996
CLASSIFICATION:
ATTORNEY APACTION:
                                                       Score 45; DB 2;
Pred. No. 0.6;
1; Mismatches (
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STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                  ; Sequence 14, Application US/08621751A
; Patent No. 5882644
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 321152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEPHONE: (650) 494-0792
TELERX: 706141 MRSN FOERS SFO
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-483-636-58
; Sequence 58, Application US/08483636
; Patent No. 594110
; GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
                                                                                                                                                                                                                                                                                                                         APPLICANT: Chang, Chung N.
APPLICANT: Landolfi, Nicholas F.
APPLICANT: Martin, Ulrich
TITLE OF INVENTION: MONOCLONAL A
TITLE OF INVENTION: METHODS OF U
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88.9%;
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88.9%;
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                                       Query Match
Best Local Similarity 88.>
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 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
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Best Local Similarity
8; Conserve
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                                                                                                                                    1 QQSSEDPPT 9
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 ; MOLECULE TYPE:
US-08-621-751A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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APPLICANT: Chang, Chung N.

APPLICANT: Chang, Chung N.

APPLICANT: Chang, Chung N.

APPLICANT: Landolfi, Nicholas F.

APPLICANT: MANUALIO, MICHOLAS F.

TITLE OF INVENTION: MANUALION: MATHODS OF USE THEREOF

TITLE OF INVENTION: MATHODS OF USE THEREOF

TITLE OF INVENTION: MATHODS OF USE THEREOF

TORRESPONDENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER LLP

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,751A
FILING DATE: 22-MAR-1996
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HALCH C.
REGISTRATION NUMBER: 25,258
REFFERENCE/DOCKET NUMBER: 53466/126/AAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: --
CLASSIFICATION:
CLASSIFICATION:
NAME: Lehnbardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 32,152000100
TELECOMMUNICATION INFORMATION:
TELEFRAM: (650) 813-560
TELEFRAM: (650) 813-560
TELEFRAM: (650) 494-0792
TELEX: 706141 MRSN FOERS SFO
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
""DOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 2
Pred. No. 0.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5390
TELERA: 904136
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 anning acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.8%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 93.8
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein 8-436-717-33
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FILING DATE: 07-SEP-PRIOR APPLICATION DATA:
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ZIP: 19406-0939
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CLASSIFICATION:
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88.9%; Pred. No. 0.6;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant II.4 Antibodies Useful in TITLE OF INVENTION: Treatment of II.4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SMithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
Recombinant IL4 Antibodies Useful in Treatment of IL4 Mediated Disorders
                                                                                                                                                                                          ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
                                    NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STRRET: P.O. Box 1539 / UW2220
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT/US/94/10308
                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/11/366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sutton, Jeffrey A.
REGISTRAILON NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFANE: (215) 270-5090
INFORMATION FOR SEQ ID NO: 58:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-483-632-58
; Sequence 58, Application US/08483632
Patent No. 5928904
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-SEP-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 131 amino acids
amino acid
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STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-483-636-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19406-0939
COMPUTER READABLE FORM:
TITLE OF INVENTION:
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nes 8; Conserv
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                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/483,636
                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 / UW2220 CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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88.9%; Pred. No. 0.6;
tive 1; Mismatches
                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION NUMBER: US 08/136783
FILING DATE: 14-0CT-1993
PRIOR APPLICATION NUMBER: US 08/136783
FILING DATE: 14-0CT-1993
PRIOR APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY AGENT INFORMATION:
NAME: SULTON, Jeffrey A.
REGISTRATION NUMBER: P50186-3
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION:
                                                                                                                            APPLICATION NUMBER: US/08/483,632
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08483636 Patent No. 5914110 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 131 amino acids TYPE: amino acid
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Best Local Similarity 86.۶۰
امر 8; Conservative
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Gaps

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APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/483,636
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
ADRESSEE: Intellectual Property
CITY: King of Prussia
                                                                                                                                                                           93.8%; Score 45; DB 2
88.9%; Pred. No. 0.6;
iive 1; Mismatches
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 07-5EP-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 14-0CT-1993
PRIOR APPLICATION DATA:
FILING DATE: 14-0CT-1993
PRIOR APPLICATION DATA:
FILING DATE: 07-5EP-1994
ATOCNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P50186-3
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28, Application US/08483636 Patent No. 5914110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5020
INFORMATION FOR SEQ ID NO: 28: SEGUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
      INFORMATION FOR SEQ ID NO: 2:
                                              : 132 amino acids
amino acid
                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                  ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-632-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                        113 QQSNEDPPT 121
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                                              LENGTH:
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Patent No. 5928904
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF SEQUENCES: 75
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property Transfer: P.O. Box 1539 / UW2220 CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
PRECORTION NUMBER: US 08/117366
FILING DATE: 07-5EP-1993
PRIOR APPLICATION DATA:
PRICATION NUMBER: US 08/136783
FILING DATE: 14-607-1993
PRIOR APPLICATION DATA:
FILING DATE: 14-607-1993
PRIOR APPLICATION DATA:
FILING DATE: 07-5EP-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                REFERENCE POCKET NUMBER: P50186-3
RELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
                                                              PCT/US/94/10308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028 REFERENCE/DOCKET NUMBER: P50186-3 TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 270-5024 TELEFAX: (215) 270-5090
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                           FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                  st Local Similarity 88.9
                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-483-636-2
                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 QQSNEDPPT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QQSSEDPPT 9
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                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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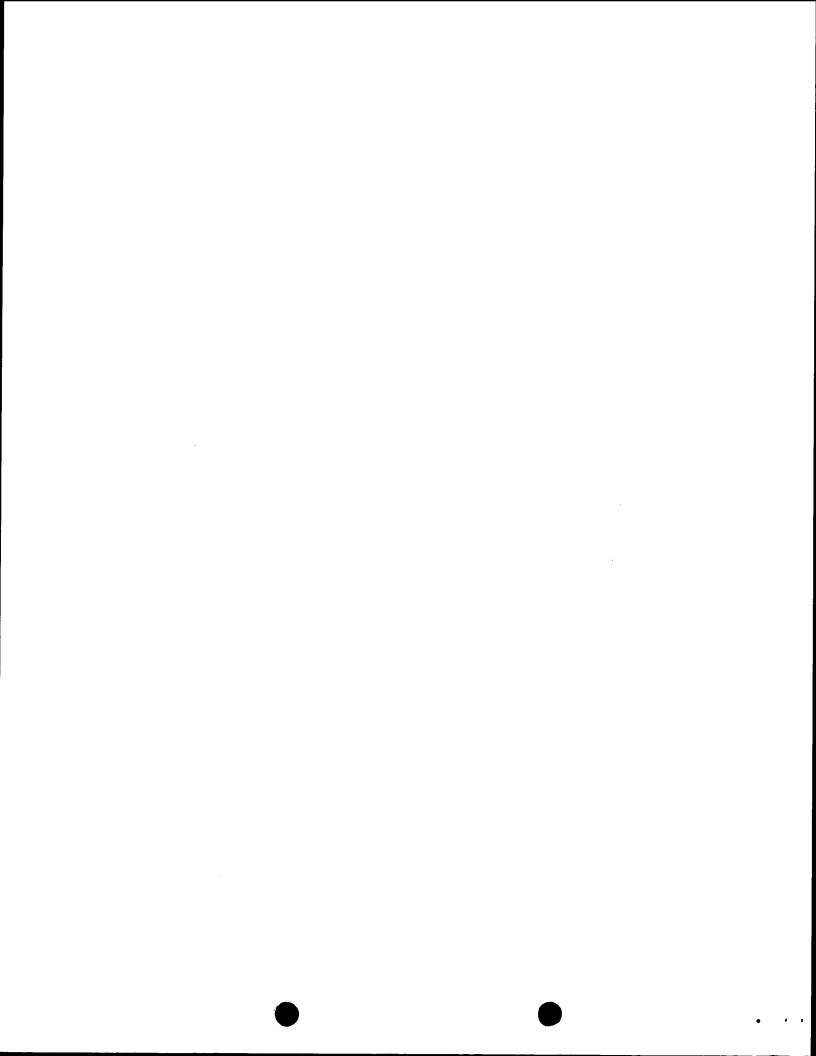
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APPLICANT: Sylvester, Daniel R.

TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCE: 75
CORRESPONDENCE ADDRESS: 75
CORRESPONDENCE ADDRESSE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: Po. Box 1539 / UW2220
CUTY: King of Prussia STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.3%; Score 40; DB 2; Length 131; 87.5%; Pred. No. 4.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: February 14, 2003, 11:20:50 Job time: 8.12903 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/11/366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION NUMBER: US 08/136/83
APPLICATION NUMBER: US 08/136/83
FILING DATE: 14-OCT-1993
PRIOR APPLICATION NUMBER: PCT/US/94/10308
APPLICATION NUMBER: PCT/US/94/10308
ATTORNEY/AGENT INFORMATION:
NAME: SULFON, Jeffrey A.
RESISTRATION NUMBER: 34,028
RESISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
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TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 131 amino acids TYPE: amino acid
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Best Local Similarity 8/...
T; Conservative
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APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: STYLES OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%; Score 40; DB 2; Length 9; 87.5%; Pred. No. 2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SmithKiline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 / UW2220 CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
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Patent No. 5914110
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
                                                                                                                                                                  Sequence 28, Application US/08483632 Patent No. 5928904 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 13406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE TO THE PER PROCESS OF TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: SULton, Jeffrey A.
REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-483-632-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QOSSEDPP 8
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                1 QQSSEDPP 8
                                       1 QOSNEDPP 8
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US-08-483-636-14
                                                                                                                          RESULT 14
US-08-483-632-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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(without alignments)
44.001 Million cell updates/sec
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2: /cgr2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgr2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
3: /cgr2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: /cgr2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
6: /cgr2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
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11: /cgr2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
12: /cgr2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
13: /cgr2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
14: /cgr2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140259 seqs, 25548876 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                US-09-701-001B-6
48
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                                                                                                                                                                                                                                                                                         Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
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                                                                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 20, Appl	Sequence 80, Appl	Sequence 58, Appl	Sequence 2, Appli	Sequence 28, Appl	Sequence 14, Appl	Sequence 2, Appli	Sequence 17, Appl	Sequence 2, Appli	Sequence 81, Appl	Sequence 36, Appl	Sequence 37, Appl	Sequence 144, App	Sequence 235, App	Sequence 236, App	Sequence 6, Appli	Sequence 6, Appli	Sequence 87, Appl	Sequence 2, Appli
	ID	US-09-879-461-20	US-09-144-886-80	US-09-879-461-58	US-09-879-461-2	US-09-879-461-28	US-09-879-461-14	US-09-881-823-2	US-10-078-650-17	US-10-094-649-2	US-09-144-886-81	US-09-810-502-36	US-09-810-502-37	US-09-771-161A-144	US-09-771-161A-235	US-09-771-161A-236	US-09-802-077-6	US-09-802-096-6	US-09-144-886-87	US-09-917-410-2
	DB	6	6	σ	6	0	6	10	6	6	6	10	10	10	10	10	10	10	σ	10
	Query Match Length DB		112	131	132	σ	131	134	412	412	112	112	112	780	942	942	106	106	112	218
	Query Match	3.8	3.8	3.8	3.8	3.3	3.3	5.0	5.0	5.0	2.9	72.9	5.9	5.9	5.9	2.9	8.0	8.0	8.0	8.0
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	Score	45	45	45	45	40	40	36	36	36	35	35	35	35	35	35	34	34	34	34
	Result No.		7	3	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19

FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: SULLOD, JOEFFERY
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2

TELECOMMUNICATION IRRORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:

APPLICATION NUMBER: 08/612,929

Sequence 1514, Ap Sequence 91, Appl. Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 9, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 12, Appli Sequence 12, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 27, Appli Sequence 27, Appli Sequence 28, Appli Sequence 86, Appli Sequence 94, Appli	ies Useful in ed Disorders ion y, UW2220 - 709 on #1.25
US-09-796-692-1514 US-10-001-888-91 US-09-802-077-2 US-09-802-077-2 US-09-920-171-6 US-09-920-171-6 US-09-920-171-9 US-09-920-171-9 US-09-920-171-10 US-09-920-171-10 US-09-920-171-10 US-09-920-171-13 US-09-920-171-13 US-09-920-171-13 US-09-920-171-13 US-09-920-171-12 US-09-920-171-12 US-09-920-171-12 US-09-920-171-22 US-09-920-171-22 US-09-920-171-23 US-09-920-171-33 US-09-920-171-33 US-09-920-171-33 US-09-920-171-33 US-09-920-171-33	ALIGNMENTS 20 Application US/09879461 No. US20020193575A1 No. US20020193575A1 CANT: Holmes, Stephen D. GGOSS, Mitchell S. Sylvester, Daniel R. OF INVENTION: Recombinant IL4 Antibodies Treatment of IL4 Mediated Treatment of IL4 Mediated SPONDENCE 58 SPONDENCE 58 SPONDENCE SE SMITCHAINE Beecham Corporation STREET: Corporate Intellectual Property, Swedeland Rd. CITY: King of Prussia STATE: PA STATE: PA TER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version NT APPLICATION DATA: CLASSIFICATION NUMBER: US/09/879,461 FILING DATE: 12-Jun-2001 CLASSIFICATION CUNKNOWD> APPLICATION NUMBER: US/09/879,461 FILING DATE: 12-Jun-2001 CLASSIFICATION CUNKNOWD>
2.8 61 9 3.8 111 10 3.8 218	ALIGNMEE -461-20 e 20, Application US/09879461 tion No. US20020193575A1 AL INCRNATION: APPLICANT: Holmes, Stephen D. Gross, Mitchell S. Sylvester, Daniel R. TITLE OF INVENTION: Recombinant IL. TITLE OF INVENTION: Recombinant IL. TREATMENT OF SEQUENCES: 58 CORRESPONDENCE: 58 CORRESPONDENCE: Anithkline Beecham STREET: Corporate Intellectua Symath Proporate Intellectua Symmath Propo
20 22 22 22 22 22 24 24 25 24 33 33 33 33 33 33 33 33 33 33 44 41 33 44 44 33 44 44 33 68 88 83 83 68 88 83 83 83 68 88 88 83 83 83 83 83 83 83 83 83 83 83	1 ence 20, ication NERAL IN APPLI TITLE CORRE CORRE
A CALACA CAL	RESULT US-09- Sequ Publ

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RESULT 4
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Patent No. US20020155114A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117050
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence: BonT/A clone; OTHER INFORMATION: 186 region VL epitope 1 US-09-144-886-80
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0
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ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 - 709
RAGGELAND RG.
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APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9; Length 112;
                                                                                                                       93.8%; Score 45; DB 9; Length 9; 88.9%; Pred. No. 1.2e+05; "viematrhes 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.8%; Score 45; DB 9;
88.9%; Pred. No. 0.28;
tive 1; Mismatches
                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-879-461-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quence 58, Application US/09879461
ublication No. US20020193575A1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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Best Local Similarity 86.5.
نمر 8; Conservative
                                                                                                                                                                                   Conservative
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                                                                                                                                                            Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 QQSNEDPPT 101
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LENGTH: 112
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Gaps
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ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 - 709
Swedeland Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment of IL4 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.8%; Score 45; DB 9; Length 131; 88.9%; Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SISTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Unn-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/136,783
ATTORNEY/AGENT INFORMATION:
MAME: SULTON: Jeffrey A.
REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/612,929
FILING DATE: cforknown>
APPLICATION NUMBER: 0S 08/136,783
FILING DATE: 14-0CT-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 58: US-09-879-461-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 131 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-879-461-2; Sequence 2, Application US/09879461; Publication No. US20020193575A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (215) 270-5090
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                                                                                                                                                                                                                                                                                                                TELEFAX: (215) 270-50
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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Best Local Similarity 88.9،
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APPLICANT: CHEN, LI IIILE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
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0
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CORRESPONDENCE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 - 709
Swedeland Rd.
CITY: King of Prussia
                                                                                                  Sequence 14, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
ITLE OF INVENTION: Treatment of IL4 Antibodies Useful in Treatment of IL4 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 131;
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87.5%; Pred. No. 2.4;
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APPLICATION NUMBER: 08/612,929
FILING DATE: «ONKNOWN»
PPLLING DATE: 14-OCT-1993
FILING DATE: 14-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: P50186-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-879-461-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (215) 270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/09881823
; Patent No. US20020068066A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (215) 270-5090 INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 131 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SHI, WENYUAN
APPLICANT: ANDERSON, MAXWELL
APPLICANT: MORRISON, SHERIE
APPLICANT: TRINH, RYAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 19406-2799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TRINH, RYAN APPLICANT: WIMS, LETITIA APPLICANT: CHEN, LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: PA
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1 QQSNEDPP
                                                                                  US-09-879-461-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in Treatment of IL4 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTY: USA

ZIP: 19406-2799

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION :
            CLASSIFICATION DATA:
            PRIOR APPLICATION DATA:

                                                                                                                                                                                              93.8%; Score 45; DB 9; Length 132; 88.9%; Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 9;
                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/612,929
FILING DATE: <Unknown>
APPLICATION NUMBER: 08 08/136,783
FILING DATE: 14-0CT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P50186-2
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-879-461-28
             SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-879-461-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
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TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Application US/09879461 Publication No. US20020193575A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Holmes, Stephen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
    INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                            113 QQSNEDPPT 121
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39-879-461-28
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Patent No. US20020155114A1

GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.1170SO
CURRENT APPLICATION NUMBER: US/09/144,886

CURRENT FILING DATE: 1998-08-31

NUMBER OF SEQ ID NOS: 98

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone COTHER INFORMATION: 1C9 region VL epitope 1 US-09-144-886-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Padlan, Eduardo A.
APPLICANT: Padlan, Eduardo A.
Daugherty, Bruce L.
Mark, George E.
TITLE OF INVENTION: A METHOD FOR REDUCING THE IMMUNOGENICITY
OF ANTIBODY VARIABLE DOMAINS
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                                                                                                                                                                             Length 412;
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COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
                                                                                                                                                                               6
                                                                                                                                                                             DB
40;
                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                           Score 36;
Pred. No. 4
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                                                                                                                                                                        75.0%;
66.7%;
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ZIP: 07065-0907
COMPUTER READABLE FORM:
                        SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2
                                                                                                                                                                                                                        6; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                            LENGTH: 412
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Rahway
    NUMBER OF SEQ ID NOS:
                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
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279 KQESEEPPT 287
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                                                                                                                                                                                                                                                                1 QQSSEDPPT 9
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US-09-144-886-81
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LENGTH: 112
                                                                                                                                  US-10-094-649-2
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US-10-094-649-2
Sequence 2, Application US/10094649
Sequence 2, Application US/10094649
Sublication No. US2003009020A1
GENERAL INFORMATION:
APPLICANT: Kawamoto, Takeshi
TITLE OF INVENTION: Gene Originating in Human Chondrocyte
FILE REPERENCE: 46124-5014-05
CURRENT APPLICATION NUMBER: US/10/094,649
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: US/09/462,624
PRIOR APPLICATION NUMBER: UP 20227/1997
PRIOR APPLICATION NUMBER: JP 202227/1997
PRIOR PILING DATE: 19997-07-11
PRIOR PILING DATE: 1998-07-10
                                                                                                                                                                                                                                                                              75.0%; Score 36; DB 10; Length 134; 66.7%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.0%; Score 36; DB 9; Length 412; 66.7%; Pred. No. 40; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                             1; Indels
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APPLICANT: Katc, Yukio
APPLICANT: Katc, Yukio
TITLE OF INVENTION: NOVEL BHLH TYPE TRANSCRIPTION FACTOR
TITLE OF INVENTION: GENES DEC2
FILE REFERENCE: 0.6501-0.1001
CURRENT APPLICATION NUMBER: US/10/078,650
CURRENT FILING DATE: 2002-02-19
                                                                                                                                                                                                                                                                                                                           2; Mismatches
               CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 07/378,577
PRIOR FILING DATE: 1999-08-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/JP00/03991
PRIOR FLILING DATE: 2000-06-19
PRIOR APPLICATION UNBER: JP 11-233286
PRIOR FILING DATE: 1999-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/10078650 Patent No. US20020169301A1
APPLICANT: Fujimoto, Katsumi
                                                                                                   NUMBER OF SEQ ID NOS: 32
SOFWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 134
                                                                                                                                                                                                                                                                                                  Best Local Similarity 66.7
Matches 6; Conservative
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FILE REFERENCE: 22851-032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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atches 6; Conserv
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|113 QQNNADPPT 121
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279 KQESEEPPT 287
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                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Murine
US-09-881-823-2
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-10-078-650-17
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                                                                                                                                                                                                                                                                                Query Match
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Pred. No. 15;
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US-09-771-161A-235
Sequence 235, Application US/09771161A
Sequence 235, Application US/09771161A
Patent No. US20020110811A1
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT APPLICATION NUMBER: 09/724,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 18410CC TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
TELEPAX: 732-594-4720
TELEX: cUnknown>
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-810-502-37
          APPLICATION NUMBER: 07/702,217
                                                                                                    NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 144, Application US/09771161A Patent No. US20020110811A1
                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 112 amino acids
                                      FILING DATE: 17-May-199
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.98;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.93
Best Local Similarity 77.83
Matches 7; Conservative
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Best Local Similarity
'-has 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEO for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILING DATE: 16-Mar-2001
CLASSIFCATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
APPLICATION NUMBER: US/09/810,502
FILING DATE: 16-Mar-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/905,280
FILING DATE: 01-Aug-1997
APPLICATION NUMBER: 08/609,218
FILING DATE: 01-Mar-1996
APPLICATION NUMBER: 08/109,187
FILING DATE: 19-Aug-1993
                                                                                                                                                                  FILING DATE: 01-Aug-1997
APPLICATION NUMBER: 08/609,218
FILING DATE: 01-War-1996
APPLICATION NUMBER: 08/109,187
FILING DATE: 19-Aug-1993
APPLICATION NUMBER: 07/702,217
FILING DATE: 17-May-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 18410CC TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                      APPLICATION NUMBER: 08/905,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Padlan, Eduardo A. Daugherty, Bruce L. Mark, George E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 37, Application US/09810502 Patent No. US20020034765A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 732-594-3905
TELEFAX: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: NJ
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72.9%; Score 35; DB 10; Length 942;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                            72.9%; Score 35; DB 10; Length 942; 66.7%; Pred. No. 1.4e+02; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-771-161A-236
Sequence 236, Application US/09771161A
Patent No. US20020110811A1
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROFEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR PRILING DATE: 2000-01-128
PRIOR FILING DATE: 2000-06-115
PRIOR PLILOGATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-115
PRIOR PLILOGATION NUMBER: 135619
PRIOR APPLICATION NUMBER: 135619
PRIOR APPLICATION NUMBER: 135619
PRIOR PRING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PALENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: February 14, 2003, 11:21:32 Job time : 6.22581 secs
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SEQ ID NO 235
LENGTH: 942
                                                                                                                                                                                                                                                                                            Query Match 72.99
Best Local Similarity 66.79
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
US-09-771-161A-236
                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-09-771-161A-235
                                                                                                                                                                                                                                                                                                                                                                                                              1:11 |||:
564 QKSSRDPPS 572
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564 QKSSRDPPS 572
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 14, 2003, 11:12:02; Search time 9 Seconds (without alignments) 96.134 Million cell updates/sec

US-09-701-001B-6 1 QQSSEDPPT 9 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues ched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

PIR_73:* Database :

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	(Query		i	1	
No.	Score	Match	Length	BB	ΩI	Description
Т	48	100.0	112	7	S19971	Id kappa chain V r
7	48	0	131	7	PH1226	Kappa
<u>س</u>	38	6	112	7	_	chain
4	38	6	301	7	585	3-MYB
2	38	79.2	304	Н	S71285	relat
9	37		508	7	F84921	\neg
7	36	δ.	65	~	C38601	kappa cha
œ	36		412	7	JC5547	
			96	~	B49442	light
10		•	102	7	PH1079	q light
		ς.	107	7	S26344	q kappa
12	35		111	Н	KVMS37	q kappa
13	35	72.9	111	-	KVMSC1	
14		S.	111	Н	KVMS83	q kappa
	35	ς.	111	~	996608	g kappa
	35		111	7	A33936	b
17	35	'n,	479	7	S48705	serine/threonine p
18	32	'n.	942	7	JC2129	protein kinase PKN
19	32	ζ,	950	7	S27473	URBS1 protein - sm
20	34	٠	107	7	S26343	Ig kappa chain V r
21	34	。	111	-	KVMS43	
22	34	•	111	Н	KVMS08	Iq kappa chain V r
23	34	ö	111	Н	KVMS69	
24	34	o.	127	7	B84172	
25	34		268	7	T51678	Ψ
56	34	70.8	320	N	C85440	
27	34		352	7	AE0034	Ω
28	34	70.8	794	7	T27870	hypothetical prote
29	34		925	7	JC2033	_

hypothetical prote	p53-binding protei	BPLF1 protein - hu	short neurotoxin 1	Iq kappa chain V r	hypothetical prote	anti-qlycoprotein	hypothetical prote	hypothetical prote	probable rmlA2 pro	voltage-gated pota	lanosterol synthas	cyclin F - human	protein kinase - s	microtubule-vesic1	restin - human
T00050	I38604	QQBE8	NIUJIM	S42193	C97796	D45722	D82539	T35200	A70978	JE0276	S46813	A55501	S49313	A43336	\$22695
7	7	7	Н	7	7	7	7	7	7	7	7	7	~	~	7
1006	1027	3149	62	81	87	111	135	192	359	491	731	786	1094	1392	1427
70.8	70.8	70.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	8.89	68.8	68.8	68.8	68.8	68.8
34	34	34	33	33	33	33	33	33	33	33	33	33	33	33	33
30	31	32	33	34	35	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment) C;Species: Was musculus (house mouse) C;Species: Was musculus (house mouse) C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000 C;Accession: S19971; S19973 R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P. Submitted to the EMBL Data Library, March 1992 A;Description: Structural characterization of CD4 mAb.
ate: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan coession: S19971; S19973 essenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P. attted to the EMBL Data Library, March 1992 escription: Structural characterization of CD4 mAb.
alssenhorn, W.; Riethmeller, G.; Weiss, E.M.; Rieber, E.P. mitted to the EMBL Data Library, March 1992 escription: Structural characterization of CD4 mAb.
nitted to the EMBL Data Library, March 1992 sscription: Structural characterization of CD4 mAb. effection under: \$19963
<pre>sscription: Structural characterization of CD4 mAb. effection of unber: \$19963</pre>
110000
SCESSION: SI99/I
A; Molecule type: mRNA
A; restudes: 1 112 < WELL A; Cross-references: EMBL: X65091: NID: 052288: PIDN: CAA46219.1: PID: 052289
A; Experimental source: clone M-T310
A; Accession: S19973
A; Molecule type: mRNA
A; Nesidades: I III /WEW/ A:Cross-references: EMBL:X65092: NID:052292: PIDN.CAA46220 1: PID.052293
A, Experimental source: M-T404
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin F;16-94/Domain: immunoglobulin homology <imm></imm>
100.08;
best botal similarity 100.0%; Fred. NO. 0.005; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps
1 QQSSEDPPT 9
93 QQSSEDPPT 101

RESULT 2

In Aappa chain precursor V region (M-T310) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: T7-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C; Accession: PH1226
R; Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; L. Gene 12, 271-278, 1992
A; Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and A; Reference number: PH1224; MUID:93077041; PMID:1446824
A; Accession: PH1226
A; Molecule type: mRNA
A; Residues: 1-131 < WEI>
A; Cross-references: GB:S50265; NID:q260765; PIDN:AAB24320.1; PID:q260766
A; Note: this mouse sequence was hybridized and fused with a human constant region gen C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin F;1-20/Domain: signal sequence #status predicted <NGS>
F;21-131/Product: Ig light chain V region #status predicted <MAT>

QQ

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Gaps

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Targets chain V region (2B5) - mouse (fragment)

Ig kappa chain V region (2B5) - mouse (fragment)

Ig kappa chain V region (2B5) - mouse (fragment)

Ig kappa chain V region (2B5) - mouse (fragment)

Is peciles: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999

C; Accession: C38601

A; Title: Common structural features among monoclonal antibodies binding the same anti

A; Reference number: A38601; MUID:91115823; PMID:1703527

A; Accession: C38601

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-65 <COS>
A; Residues: 1-65 <COS>
A; Cross-references: GB:M57980; NID:9196406; PIDN:AAA63361.1; PID:9196407

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:254137; NID:91263096; PIDN:CAA90810.1; PID:91263097
C;Superfamily: Arabidopsis myb-related 33.2K protein; myb DNA-binding repeat homology
C;Keywords: DNA binding; duplication
F;1-52/Domain: myb DNA-binding repeat homology <MXBl>
F;53-103/Domain: myb DNA-binding repeat homology <MXB2>
                                      C;Accession: S71285
R;Kirik, V.; Bamulein, H.
Submitted to the EMBL Data Library, September 1995
A;Description: Characterization of two cDNAs encoding MYB-related proteins in Arabido
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE002093; NID:g3738308; PIDN:AAC63650.1; GSPDB:GN00139 C;Genetics:
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 16-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 1; Length 304;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 508;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.2%; Scor.
100.0%; Pred. No. ...
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Pred. No. 33;
2; Mismatches
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66.78;
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Best Local Similarity 100.0
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                           A; Reference number: S71285
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241 EDSTEDPPT 249
                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-304 <KIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QQSSEDPPT 9
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                                                                                                                                                                                                                 A; Accession: S71285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: At2947960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 2
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submitted to the Protein Sequence Database, December 1999
A;Reference number: 223007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Map position: 3
A,Note: F3A4.140
C,Superfamily: Arabidopsis myb-related 33.2K protein; myb DNA-binding repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
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$19972
$19972
[I kappa chain V region (M-T321) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mos musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession; S1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession; S1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S19963
A;Reference number: S19963
A;Reference number: S19963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: protein F3A4.140
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Mar-2000
C;Accession: T45859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL:X65094; NID:q52290; PIDN:CAA46222.1; PID:q52291 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F;16-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                         100.0%; Score 48; DB 2; Length 131; 100.0%; Pred. No. 0.066; 1. Indels 1. In
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Pred. No. 4.2;
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Alecule type: DNA
A; Residues: 1-301 <BAR>
A; Cross-references: EMBL:AL132978
A; Experimental source: cultivar Columbia; BAC clone F3A4
C; Genetics:
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T45859
R2R3-WYB transcription factor - Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              imyb-related protein, 33.2K - Arabidopsis thaliana (C. Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
             F;36-114/Domain: immunoglobulin homology <IMM>
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88.9%;
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Best Local Similarity 100.0
Matches 7; Conservative
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                                                                                                                                                      Conservative
                                                Query Match
Best Local Similarity
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Aydolecule type: mRNA
A;Residues: 1-112 <WEI>
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                              113 QOSSEDPPT 121
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C,Accession: S2634
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 1-111 <WEI>
R; McKean, D.J.; Bell, M.; Potter, M.
R; McKean, D.J.; Bell, M.; Potter, M.
A; Title: Mechanisms of antibody diversity; multiple genes encode structurally related
A; Reference number: A93822; MUID:79012520; PMID:99744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light ( hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Rearrangement of genetic information may produce immunoglobulin diversity. A;Reference number: A93204; MUID:79073152; PMID:103003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 21-Jan-2000
C;Accession: A93204; A93822; A01934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Cross-references: EMBL:X59209; NID:g52336; PIDN:CAA41919.1; PID:g1334074 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F:15-93/Domain: immunoglobulin homology <IMM>
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                               A;Residues: 1-102 <TIL>
A;Residues: 1-102 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                       Length 102
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Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce i
                                                                                                                                                                                                    72.9%; Score 35; DB 2; 77.8%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
15;
                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                             F:16-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Mus musculus (house mouse)
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77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain V region - mouse
                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                              Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-107 <STA>
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                                                                                                                                                                                                                                                                                                                                                  ||| | |||
93 QOSKEVPPT 101
                                                                                                                                                                                                                                                                                                                  1 QQSSEDPPT 9
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           A; Molecule type: mRNA
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                                                                                                                                                                                                       Query Match
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R;Shen, M.; Kawamoto, T.; Yan, W.; Nakamasu, K.; Tamagami, M.; Koyano, Y.; Noshiro, M.;

Biochem. Biophys. Res. Commun. 236, 294-298, 1997

A;Title: Molecular characterization of the novel basic helix-loop-helix protein DEC1 exp

A;Fitle: Molecular characterization of the novel basic helix-loop-helix protein DEC1 exp

A;Fitle: Molecular characterization of the novel basic helix-loop-helix protein DEC1 exp

A;Fitle: Molecular C5547, MUID:97382424; PMID:9240428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: DDBJ:AB004066; NID:92308996; PIDN:BAA21720.1; PID:92308997
C; Comment: This protein is involved in the control of cell differentiation in several ti
F;51-108/Region: helix-loop-helix #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ristura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapie, L.M.; Sproteins 14, 499-508, 1992
A;Title: Crystallization, sequence, and preliminary crystallographic data for an antipep A;Reference number: A49442; MUID:93066166; PMID:1438187
A;Accession: B49442
A;Status: preliminary; not compared with conceptual translation plecule type: DNA
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Cispecies: Mus musculus (house mouse)
Cispecies: 30-5ep-1993 #sequence_revision 30-5ep-1993 #text_change 21-Jan-2000
Cinccession: PH1079
Cinccession: PH1079
Cinccession: PH1079
Cinccession: PH1079
Cinccession: PH0071; Multi, R.J.; Marion, T.N.
Cinccession: PH0071; Multiple and the products of clonally selective Affecence number: PH0971; Multiple Affecession: PH1079
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                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig light chain V region (50.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 96;
                                  Indels
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66.7%; Pred. No. 40,
... 2; Mismatches
                               Mismatches
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;8-86/Domain: immunoglobulin homology <IMM>
        Pred. No.
                                                                                                                                                                                                                                                                                     basic helix-loop-helix factor DEC1 - human
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77.8%;
  77.8%;
                                  Conservative
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Best Local Similarity
Matches 6; Conserv
Best Local Similarity
Matches 7; Conserv
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85 QQSNEDPLT 93
                                                                                                                                             QOSNEDPRT 54
                                                                                      1 QOSSEDPPT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QQSSEDPPT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QOSSEDPPT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Gaps

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Search completed: February 14, 2003, 11:19:48 Job time : 10 secs
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30.Nov-1980 #sequence_revision 30.Nov-1980 #text_change 31-Mar-2000
C;Accession: A01936
R;McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A;Title: Mechanisms of antibody diversity: multiple genes encode structurally related mc
A;Reference number: A03822; MuID:79012520; PMID:99744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin P;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                             G;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C;Accession: B01937; A01937
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
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C.Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
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  Score 35; DB 1; Length 111; Pred. No. 15;
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Pred. No. 15;
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72.9%;
77.8%;
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77.8%;
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
                 Best Local Similarity 77.8 Matches 7; Conservative
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sidues: 1-111 <WEI>
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Best Local Similarity
Matches 7; Conserv
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93 QOSNEDPLT 101
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| 93 QQSNEDPYT 101
                                                                                      1 QQSSEDPPT 9
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      Query Match
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KVMS83
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S09966
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KVMSC1
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C;Accession: S09966
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A;Titler. Variable region sequences of pathogenic anti-mouse red blood cell autoantibo A;Reference number: S09955; MUID:90269328; PMID:2347362
A;Accession: S09966
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                          A;Cross-references: EMBL:X51854; NID:955397; PIDN:CAA36147.1; PID:9930231
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                     F;16-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-111 <REI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 QQSNEDPYT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QQSSEDPPT 9
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

February 14, 2003, 11:05:27 ; Search time 4.64516 Seconds (without alignments) 80.360 Million cell updates/sec Run on:

US-09-701-001B-6 48 1 QOSSEDPPT 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues :pəq:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cription	O35185 mus musculu		homo sa	m snm		snu	рошо	ustil	-	mus	P01669 mus musculu	P05901 human immun	Q99865 homo sapien	antho		epst			O88396 mus musculu	Q15642 homo sapien		P41002 homo sapien	_	Q9epv5 rattus norv	P30622 homo sapien	P01662 mus musculu	P01663 mus musculu	P09711 human cytom		49	866	988	000515 homo sapien
SUMMARIES		BHB2_MOUSE	BHB2_RAT	BHB2_HUMAN	KV3H_MOUSE	KV3L_MOUSE	KV3N_MOUSE	PKL1_HUMAN	URB1_USTMA	KV3M_MOUSE	KV30_MOUSE	KV3Q_MOUSE	VIF_HV2NZ	SPIH_HUMAN	GLHR_ANTEL	P531_HUMAN	TEGU_EBV	NXS1_NAJMO	REV_HV1LW	GRE2_MOUSE	CIP4_HUMAN	ERG7_YEAST	CG2F_HUMAN	APAF_MOUSE	APAF_RAT	REST_HUMAN	KV3J_MOUSE	KV3K_MOUSE	J1I_HCMVA	P53_ICTPU	SHBG_MOUSE	SOXC_RHOSO	UBPB_CANFA	LAD1_HUMAN
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df	Query	75	75.0	75.0	72.9	72.9	72.9	72.9	72.9	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	68.8	68.8	8.89	68.8	68.8	8.89	68.8	68.8	68.8	2.99	66.7	66.7	66.7	2.99	2.99	66.7	66.7
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Q9umx9 homo sapien	P45897 caenorhabdi	P20794 homo sapien	O61545 mus musculu	Q01844 homo sapien	P24482 saccharomyc	060446 cricetulus	092598 homo sapien	O61699 mus musculu	P52593 saccharomyc	P07293 oryctolagus	
MATP_HUMAN	SMA4_CAEEL	MAK_HUMAN	EWS_MOUSE	EWS_HUMAN	DPB2_YEAST	H105_CRIGR	H105_HUMAN	H105_MOUSE	N188_YEAST	CCAS_RABIT	REPI_ECOLI
7	Н	Н	П	П	٦		Н	Н	,	,	Н
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66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	64.6
32	32	32	32	32	32	32	32	32	32	32	31
34	32	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

us-09-701-001b-6.rsp

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-!- SIMILARITY: CONTAINS 1 ORANGE DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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279 KQESEEPPT 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                   DNA_BIND
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    Qγ
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                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SUBCELLULAR LOCATION: Nuclear (By similarity).
-:- TISSUE SPECIFICITY: Expressed in heart, brain, spleen, lung, liver, muscle, kidney, uterus and gut.
-:- SIMILARITY: BELOKGY TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS.
                             INDUCTION: Stimulated by retinoic acid (RA). SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Class B basic helix-loop-helix protein 2 (bHLHB2) (Enhancer-of-split
BHLHB2 OR SHARP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASIC DÓMAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: May function as a transcriptional factor for neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Sprague-Dawley; TISSUE-Hippocampus;
BDLINE-98193761: PubMed-9532582.
Rossner M.J., Doerr J., Gass P., Schwab M.H., Nave K.-A.;
"SHARPS: mammalian enhancer-of-split- and hairy-related proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: Able to homodimerize or heterodimerize with E47 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 1; Length 411;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> T (IN REF. 2).
B392893CD49292BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 14;
2; Mismatches
                                                                                         -!- SIMILARITY: CONTAINS 1 ORANGE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coupled to neuronal stimulation."; Mol. Cell. Neurosci. 10:460-475(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORANGE.
        expressed in developing muscle.
                                                                                                                                                                                                                                                                                                          EMBL; AF010305; AAB64228.1; ---
EMBL; Y07836; CAA69165.1; ---
EMBL; AF584051; AAK50859.1; ---
EMBL; BC010720; AAH10720.1; ---
MGD; MGI:1097714; Bhlhb2.
InterPro; IPR001092; HLH_basic.
InterPro; IPR003650; Orange.
PF00010; HLH; 1.
PFAm; PF00010; HLH; 1.
SMART; SM00351; IRH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45360 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00038; HLH_1; 1. PROSITE; PS50888; HLH_2; 1.
                                                                         FRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184
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411 AA;
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279 KQESEEPPT 287
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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014503; Q96TD3;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last sequence update)
16-JUN-2002 (Rel. 41, Last sequence update)
17-JUN-2002 (Rel. 41, Last sequence update)
18-JUN-2002 (Rel. 41, Last sequence upda
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MEDITINE=21125593; PubMed=11226878;
MEDITINE=21125593; PubMed=11226878;
Teramorto M., Nakamasu K., Noshiro M., Matsuda Y., Gotoh O., Shen M.,
Tsutsumi S., Kawamoto T., Iwamoto Y., Kato Y.;
Tsutsumi S., Kawamoto T., Iwamoto Y., Kato Y.;
"Gene structure and chromosomal location of a human bHiH
"Gene structure and chromosomal location of a human bHiH
Transcriptional factor DEC1 x Stral3 x SHARP-2/BHIHB2.";
J. Blochem. 129:391-396(2001).
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HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shen M., Kawamoto T., Yan W., Nakamasu K., Tamagami M., Koyano Y.,
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InterPro; IPR001092; HLL basic.
Pfam: PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
PROSITE; PS00038; HLH_1; 1.
PROSITE; PS00038; HLH_1; 1.
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MEDLINE=97382424; PubMed=9240428;
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KV3L_MOUSE
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                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                             -!- PTM: Association with UBC9 may target the protein for proteolysis by the ubiquitin-dependent proteasome pathway.
-!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
                 "Regulation of STRA13 by the von Hippel-Lindau tumor suppressor protein, hypoxia, and the UBC9/ubiquitin proteasome degradation pathway.";
J. Biol. Chem. 276:15306-15315(2001).
I. FUNCTION: May function as a transcriptional factor to modulate chondrogenesis in response to the CAMP pathway.
Interacts with ubiquitin-conjugating enzyme (UBC9).
Interacts with ubiquitin-conjugating enzyme (UBC9).
ISUBCELLULAR LOCATION: Nuclear.
ITISSUE SPECIFICITY: Expressed in cartilage, spleen, intestine, lung, and to a lesser extent in heart, brain, liver, muscle and
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 3741/TEPC 111.
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                                                                                                                                                                                                                                                                                                                                                 EMBL, AB004066; BAA21720.1; -.
EMBL, AB043885; BAB18565.1; -.
EMBL, AF353635; AAK49525.1; -.
EMBL, AF353634; AAK49525.1; JOINED.
Genew, HGNC:1046; BHLHB2.
          MEDLINE=21226780; PubMed=11278694;
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MEDLINE=79073152; PubMed=103003;
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InterPro; IPR003650; Orange.
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21-JUL-1986 (Rel. 01, Last seq
15-JUL-1999 (Rel. 38, Last anno
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412 AA; 45510 MW;
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SMART; SM00511; ORANGE; 1.
PROSITE; PS00038; HLH_1; 1.
PROSITE; PS50888; HLH_2; 1.
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Best Local Similarity
Matches 6; Conserv
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279 KQESEEPPT 287
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DNA_BIND 53
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                                                                                                                                                                     stomach.
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P01660;
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SEQUENCE
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MEDLINE-79(12520; PubMed=99744;
MCKean D.J., Bell M., Potter M.;
McKean D.J., Rody averiable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-!- MISCELLARBOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
HSSP; PO1679; ZFBJ.
HSSP; PO1679; ZFBJ.
InterPro: IPR003506; Ig_W.
Ffam: PF00047; ig_1l.
SMART; SM00406; IGv; l.
Inmunoglobulin V region.
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"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.":
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-! MRSCELLANDOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
PIR., A01936; KWMSCI.
HSSP; P80362; lWTL.
InterPro; IPR0030366; Ig_MC.
Pfam; PF00047; ig; 1.
SMART; SM00406; IG*.
Immunoglobulin V region.
PRAMEWORK-1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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12099 MW; EC46C9D259213BE4 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-III region CBPC 101.
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                                                                Nature 276:785-790(1978)
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                                                                                                            SEQUENCE (TEPC 111)
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016512; 015143;
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-211ke I (EC 2.7.1..) (Protein-kinase C-related kinase Protein kinase C-like PKN) (Serine-threonine protein kinase N).
PRKCLI OR PRKI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.9%; Score 35; DB 1; Length 111; 77.8%; Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                         Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                1; Indels
 23 92 BY SIMILARITY.
111 111
111 AA; 11964 MW; E2B1AD98AD965962 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11952 MW; 2058BB50CE306D31 CRC64;
                                                                       / Match 72.9%; Score 35; DB 1; Local Similarity 77.8%; Pred. No. 4.9; nes 7; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region PC 7183.
                                                                                                                                                                                                                                                                                       111 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=79073152; PubMed=103003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 276;785-790(1978).
PIR: B01937; KVMS83.
HSSP, P01679; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
SMART; SM00440; Ig; I.
Immunoglobulin V region.
DOMAIN
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                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 AA;
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nes 7; Conserv
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93 QOSNEDPLT 101
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                     NON_TER
SEQUENCE
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SUBCELLULAR, LOCATION: CYtOplasmic (By similarity).
-:- TISSUE SPECIFICITY: FOUND UBIQUITOUSLY. EXPRESSED IN HEART, BRAIN, PLACENTA, LONG, SRELETAL MUSCLE, KINDEY, AND PANCREAS.
-:- PTM: AUTOPHOSPHORYLATED: PREFERABLY IN SERINE.
-:- PTM: ACTIVATED BY LIMITED PROTEOLYSIS WITH TRYPSIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A novel protein kinase with leucine zipper-like sequences: its catalytic domain is highly homologous to that of protein kinase C."; Biochem. Biophys. Res. Commun. 199:897-904 (1994).
-!- FUNCTION: CAN PHOSPHORIALE RIBOSOMAL PROTEIN S6. MEDIATES GTPASE RHO DEPENDENT INTRACELLULAR SIGNALLING (BY SIMILARITY).
-!- ENZYME REGULATION: ACTIVATED BY LIPIDS, PARTICULARLY CARDIOLIPIN AND TO A LESSER EXTENT BY OTHER ACIDIC PHOSPHOLIPIDS (BY
                                                                                                                                                                                                                                                                                                    TISSUE=Fetal brain;
MEDLINE=95154310; PubMed=7851406;
Palmer R.H., Ridden J., Parker P.J.;
"Cloning and expression patterns of two members of a novel protein-kinase-C-related kinase family.";
                                                                MEDLINE-95080426; PubMed-7988719;
Palmer R.H., Ridden J., Parker P.J.;
"Identification of multiple, novel, protein kinase C-related gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
PKC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; ATP-binding; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN KINASE.
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SMART; SM00074; HR1; 3.
SMART; SM00133; S_TK_X; 1.
SMART; SM00120; S_TKC; 1.
PROSTTE; PS00100; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR000719; Euk_pkinase.
Interpro; IPR000961; Pkinase_C.
Interpro; IPR000861; REM_repeat.
Interpro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
Pfam; PF000433; pkinase_C; 1.
Pfam; PF00183; Pkinase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eur. J. Biochem. 227:344-351(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Hippocampus;
MEDLINE=94183274; PubMed=8135837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000001; Euk_pkinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:9405; PRKCL1.
                                                                                                                                                                           products.";
FEBS Lett. 356:5-8(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000008; C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          874
629
644
740
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mukai H., Ono Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphorylation
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Gaps

0;

Indels

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d. No. 53; Mismatches

85.7%; Pred. No.

6; Conservative

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Best Local Similarity
Matches 6; Conserva
                                                                        448 OTSEDPP 454
                                              2 QSSEDPP 8
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                              Voisard C.P., Wang J., McEvoy J.L., Xu P., Leong S.A.;
"urbs1, a gene regulating siderophore biosynthesis in Ustilago
maydis, encodes a protein similar to the erythroid transcription
factor GATA-1.";
Mol. Cell. Biol. 13:7091-7100(1993).
'! FUNCTION: INVOLVED IN THE REGULATION OF SECRETED FERRICHROME-TYPE
SIDEROPHORES. ACTS DIRECTLY OR INDIRECTLY TO REPRESS THE
BIOSYNTHESIS OF SIDEROPHORES.
'! SUBCELLULAR LOCATION: Nuclear (Probable).
'! SIMILARITY: CONTAINS 2 GATA-TYPE ZINC FINGERS.
                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRODG19; GATAZNFINGER.
SMART; SM00401; ZnF_GATA; 2.
PROSTITE; PS00344; GATA_ZN_FINGER_1; 2.
PROSTITE; PS50114; GATA_ZN_FINGER_2; 2.
DNA_binding; Zinc-finger; Transcription regulation; Repressor;
                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBI_TaxID=5270;
K->R: SUBSTANTIAL REDUCTION OF AUTOPHOSPHORYLATION.
                                                              72.9%; Score 35; DB 1; Length 942; 66.7%; Pred. No. 53; 1; Indels Live 2; Mismatches 1; Indels
                          191 D -> G (IN REF. 3).
103989 MW; A89E40DCAEF560E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F969C6DA09A78C12 CRC64;
                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Siderophore biosynthesis regulatory protein URBS1.
                                                                                                                                                                                                                950 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATA-TYPE 1.
GATA-TYPE 2.
POLY-ALA.
POLY-SER.
POLY-THR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-SER
                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94019380; PubMed=8413298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, M80547; AAB05617.1; -.
PIT; S27473; S27473.
HSSP; P17679; 1GNF.
TRANSFAC; T02406; -.
InterPro; IPR000679; Znf GATA.
InterPro; IPR001164; hRIP_like.
Pfam: PF00320; GATA; 2.
                                                                                                                                                                                                                                      (Rel. 31, Created)
(Rel. 31, Last sequ
(Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101427 MW;
                                                                                                                                                                                                                                                                                                         Ustilago maydis (Smut fungus).
                                                             Query Match 72.9
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                              STANDARD;
 644
                                       942 AA;
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564 QKSSRDPPS 572
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902
950 AA;
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                                                                                                                                                                                                            URB1_USTMA
P40349;
                                     SEQUENCE
                          CONFLICT
MUTAGEN
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URB1_USTMA
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CCC
DR
DDR
DDR
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Length 950;

DB 1;

Score 35;

72.98;

Query Match

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Gaps
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                      SEQUENCE.
MEDLINE-79073152; PubMed-103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 1; Length 111; Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 7043.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 6308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAMEWORK - 2
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                              21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                           PIR; A01937; KVMS43.
HSSP; P80362; IWTL.
INTECPTO; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.88;
77.88;
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   STANDARD;
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Nature 276:785-790(1978).
                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00406; IGv; 1.
Immunoglobulin V region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 AA;
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Best Local Similarity
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                                                                                                                                                         NCBI_TaxID=10090;
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P01665;
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                                                                                                                                                                                                                                                                                                                                                                  Weigert M., Garmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 1; Length 111;
Pred. No. 7.7;
                                                                     COMPLEMENTARITY - DETERMINING-1.
                                                                                      COMPLEMENTARITY - DETERMINING - 2.
                                                                                                      COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                         70.8%; Score 34; DB 1; Length 111; 77.8%; Pred. No. 7.7;
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                                                                                                                                         12071 MW; 7A4ADE4D6C256D29 CRC64;
                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 7769.
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                                                                                                                                                                             1; Mismatches
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                                                                                                               FRAMEWORK-4.
                                                               FRAMEWORK-1.
                                                                                 FRAMEWORK-2
                                                                                                 FRAMEWORK-3
                                                                                                                                                                                                                                                                                                                                                            MEDLINE=79073152; PubMed=103003;
                InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; I.
SMART; SM00406; IGv; I.
Immunoglobulin V region.
DOMAIN
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77.8%;
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PIR, E01937; KVMS69.

HSSP, P80362: 1WTL.

InterPro; IPR003306; Ig_MHC.

InterPro; IPR003596; Ig_V.
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111 AA;
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    PIR; C01937; KVMS08.
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              HSSP; P80362; 1WTL.
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P01669;
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                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=88320359; PubMed=3261862; M.S. Jr., Collalti E., Starcich B.R., Zagury J.F., Franchini G., Reitz M.S. Jr., Collalti E., Laure F., Hall L., Fargnoli K., Jagodzinski L.L., Guo H.-G., Laure F., Arya S.K., Josephs S.F., Zagury D., Wong-Staal F., Gallo R.C.; "Genetic variability between isolates of human immunodeficiency virus "Genetic variability between isolates of human immunodeficiency virus (HIV) type 2 is comparable to the variability among HIV type 1."; Proc. Natl. Acad. Sci. U.S.A. 85:5941-5945(1988).
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MEDLINE=97419273; PubMed=9271673;
Laval S.H., Reed V., Blair H.J., Boyd Y.;
"The Structure of DXF34, a human X-linked sequence family with homology to a transcribed mouse Y-linked repeat.";
Mamm. Genome 8:689-691(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                Human immunodeficiency virus type 2 (isolate NIH-2) (HIV-2). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.8%; Score 34; DB 1; Length 215; 66.7%; Pred. No. 16; 2; Indels Live 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 AA; 25321 MW; 9B4A1F36A9690BFC CRC64;
                                                                                 01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
01-JUL-1993 (Rel. 26, Last annotation update)
virion infectivity factor (SOR protein) (Q protein).
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                      215 AA.
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PRINTS; PR00349; VIRIONINFECT.
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                          STANDARD;
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SEQUENCE FROM N.A.
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Matches 6; Conserv
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P05901;
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VIF_HV2NZ
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SM00370; LRR; 2
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Q12888;
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16-OCT-2001 (Rel. 40, Last annotation update)
Probable glycoprotein hormone G-protein coupled receptor precursor.
Anthopleura elegantissima (Sea anemone).
Eukaryota: Metazoa; Chidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94107299; PubMed=8280121; McLhacker H.-P., Grimmelikhuijzen C.J.P.; Northacker H.-P., Grimmelikhuijzen C.J.P.; Molecular cloning of novel, putative G protein-coupled receptor from sea anemones structurally related to members of the FSH, TSH, LH/CG receptor family from mammals.";
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-> A (IN REF. 2; CAA18149).
093E7E9F5340BF71 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE SPIN / STSY FAMILY
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PIR; JC2033, JC2033.
Interpro; IPR000276; GPCR_Rhodpsn.
Interpro; IPR001611; IRR.
Interpro; IPR001611; IRR.
Interpro; IPR003522; IRR_out.
Pfam; PF00001; 7fm_1; 1.
Pfam; PF00560; IRR; 6.
                                                                                                                                                                                                                                                                                 EMBL, AL022157; CAA18148.1; -.
EMBL, AL022157; CAA18149.1; -.
InterPro, IPR003671; Spin_Ssty.
Pfam; PF02513; Spin_Ssty; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26536 MW;
                                                                                                                                                                                                                                                           EMBL; Y09858; CAA70988.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z28332; CAA82186.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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208
232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                               Developmental
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P35409;
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MOD_RES
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Gaps
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MEDILTNE-94286584; PubMed-806121;
TWADUCHI K., Bartel P.L., Li B., Marraccino R., Fields S.;
"Two cellular proteins that bind to wild-type but not mutant p53.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
PROSITE; PS00237; G_PROTEIN_RECEP_FI_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_FI_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing; Repeat.
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MEDLINE=98421532; PubMed=9748285;
Trablchi K., Li B., Massa H.F., Trask B.J., Date T., Fields S.;
Trabluchi K., Li B., Massa H.F., Trask B.J., Date T., Fields S.;
"Stimulation of p53-mediated transcriptional activation by the p53-binding proteins, 53BPl and 53BP2.";
J. Biol. Chem. 273:26061-26068(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
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5 X APPROXIMATE TANDEM REPEATS.

1 (INCOMPLETE).

3.

4 (INCOMPLETE).

5 (INCOMPLETE).

N-LINKED (GLCNAC. . .) (POTENTIAL N-LINKED (GLCNAC. . . ) (POTENTIAL N-LINKED (GLCN
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17 mor suppressor p53-binding protein 1 (p53-binding protein 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 1; Length 925;
Pred. No. 80;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISOFORM).
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EXTRACELLULAR (POTENTIAL).
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7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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                                                                                                                                                                                                                                                                                                                          COUPLED RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1972 AA.
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75.0%;
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Search completed: February 14, 2003, 11:16:24 Job time : 5.64516 secs

4 SEDPPT 9 ||||||| 1050 SEDPPT 1055

δy

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Compugen Ltd.
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compue
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OM protein - protein search, using sw model

February 14, 2003, 11:10:17; Search time 18.7258 Seconds (without alignments) 99.030 Million cell updates/sec Run on:

US-09-701-001B-6 48 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1 QOSSEDPPT 9

Sequence:

Title:

671580 seqs, 206047115 residues ched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SPTREMBL_21:* Database

sp_vertebrate:*
sp_unclassified:* sp_invertebrate:* sp_rvirus:*
sp_bacteriap:* sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:* sp_organelle:* sp_archeap:* sp_plant:* sp_rodent:* sp_virus:* sp_mammal:* sp_mhc:* sp_phage:* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMARIES	
Result		* Query				
No.	Score	Match	Match Length DB	DB	ΠD	Description
н	38	79.2		10	Q9SN12	Q9sn12 arabidopsis
7	38	79.2		10	049745	049745 arabidopsis
3	38	79.2		10	039155	Q39155 arabidopsis
4	38	79.2		11	Q9CTV2	Q9ctv2 mus musculu
Ŋ	37	77.1		10	082263	082263 arabidopsis
9	35	72.9		10	Q8SA13	Q8sal3 oryza sativ
7	35	72.9			08sns0	Q8sus0 encephalito
8	35	72.9			Q9FDW1	Q9fdwl arabidopsis
6	35	72.9	305	10	Q941B3	Q941b3 arabidopsis
10	35	72.9			015523	Q15523 homo sapien
11	35	72.9			760660	Q99j97 mus musculu
12	35	72.9	-	Ŋ	Q9W3X2	Q9w3x2 drosophila
13	35	72.9		10	Q9C5K1	09c5kl arabidopsis
14	35	72.9		10	Q9FPT1	Q9fpt1 arabidopsis
15	35	72.9		10	Q9FG10	Q9fq10 arabidopsis
16	35	72.9		11	099MS7	099ms7 mus musculu

> → T	040		7	095va5 drosophila 09vsk5 drosophila 09nkx6 drosophila 08t9n4 drosophila 086jp6 homo sapien 08wxq6 homo sapien 096p79 homo sapien
0 00	10 023160 13 0908W4 16 082J49 5 08T263 4 09BZI8	4 Q9HJJ1 10 Q9FFK3 12 Q85056 5 Q95ZI5 5 Q23501		5 099VA5 5 09VSK5 5 09VBX6 5 08T9N4 4 086CP6 4 096P79 12 08V2A4
96 127 227 258 258	320 333 355 417 452	476 556 652 706 761	1051 1051 1138 1338	1608 1963 1966 1985 2813 2817 3179
70.8 70.8 70.8 70.8	70.8 70.8 70.8 70.8	70.8 70.8 70.8	70.8 70.8 70.8 70.8	70.8 70.8 70.8 70.8 70.8 70.8
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	, w w w w w w	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~
17 18 19 20 21	. 52 52 52 52 52 54 7	27 28 30 31	4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	4444 338

ALIGNMENTS

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Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                     F3A4.140.

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
Bargues M., Collado M.C., Navarro P., Terol J., Perez-Alonso M.,
Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (Nov-1999) to the EMBL/GenBank/PDBB databases.
                                                                                                                                                                                                                                                                                                                                                                                                                   EU Arabidopsis sequencing project;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL; AL1329'8; CAB62114.1; -.
                                                   Q9SN12;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
R2R3-MYB transcription factor (AT3950060/F3A4_140).
                                       301 AA
                                       PRT;
                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                     Q9SN12
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RESULT 1
                    09SN12
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Fri Feb 14 15:01:00 2003

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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceee; Arabidopsis.
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0
                                                                                                                                                                                                                                                                 79.2%; Score 38; DB 10; Length 301; 100.0%; Pred. No. 10; ive 0; Mismatches 0; Indels
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                                                                                              PROSITE; PS00037; MYB_1; 1.
PROSITE; PS00034; MYB_2; UNKNOWN_2.
PROSITE; PS50090; MYB_3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 301 AA; 33111 MW; 9CCD5863E9D06DEC CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
R2R3-MYB transcription factor.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 304 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 AA.
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                      InterPro; IPR01005; Myb_DNA_binding. Pfam; PF00249; myb_DNA-binding; 2. SMART; SM00395; SANT; 2.
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VARIANT 136 136
VARIANT 298 298
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Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                            Best_Local Similarity 100.
Matches 7; Conservative
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HSSP; P01103; 1POM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        197 SSEDPPT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
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SEQUENCE
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TRAIN=C57BL/60; TISSUE=THYMUS;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,

Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojbori T., Bono H., Ksukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lowis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Rinqwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch

Ryanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Narabar S., Wang K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 10; Length 304; Pred. No. 10;
                                                                      STRAIN-LANDSBERG ERECTA, TISSUE-SILIQUES;
BUDLINE-88341717; PubMed-9678577;
Kirlk V., Kolle K., Missera S., Baumlein H.;
"Two novel MYB homologues with changed expression in late
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                            embryogenesis-defective Arabidopsis mutants.",
Plant Mol. Biol. 37:819-827(1998).
-! SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-! SUBLIARITY: CONTAINS 2 MYB-LIKE DOWAINS.
EMBL, 254137; CAA90810.1; -.
TRANSPAC; PO1103; 1POM.
TRANSPAC; 102590; -.
InterPro; IPR001005; Myb_DNA_binding.
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100.0%; Pred. No....
0; Mismatches
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01-JUN-2002 (TrEMBLrel. 21, Last s
4933434L15R1k protein (Fragment).
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EMBL; AK020021; BAB31969.1; -.
GMC). MGI:1914803; 4933434L15Rik.
INTERFPC). IPR004046; GST_CTERM.
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Matches 7; Conservative
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                                                        SEQUENCE FROM N.A.
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246 EDSTEDPPT 254
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93 QHNSEDPP 100
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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Haysshizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Phan P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Camada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M., Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yanmaura Y., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Rawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Shinn P., Southwick A., Shinozaki K., Full Length cDNa of gene At2947960 (GI:15227177).";
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CV. COLUMBIA;
Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Expressed protein (At2947960/T9J23.10) (Hypothetical 49.3 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.
                                                                   79.2%; Score 38; DB 11; Length 564; 77.8%; Pred. No. 19;
                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lin X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                        SEQUENCE 564 AA; 62710 MW; 8EAF7A27E35B53DA CRC64;
                                                                                                                                                                                                                         442 AA
                                                                                             1; Mismatches
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InterPro; IPR000051; SAM_bind.
Pfam; PF00043; GST_C; 1.
NON_TER 1
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STRAIN-CV. COLUMBIA;
TOWN C.D., Kaul S.;
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                                                                                   Best Local Similarity
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94 QESSEHPPT 102
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                                                                                                                       1 QQSSEDPPT 9
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                                                                      Query Match
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082263
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Gaps
Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I., Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C., Fraser C.M., Venter J.C.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005309; AAC63650.2; -.
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group).
Bukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0703B11.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003302; BAB82286.1; -.
SEQUENCE 265 AA; 29807 MW; C779784F75C06E7F CRC64;
                                                                                                                                                                                                                                                                                                 77.1%; Score 37; DB 10; Length 442; 66.7%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.9%; Score 35; DB 10; Length 265; 75.0%; Pred. No. 36;
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Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon
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                                                                                                                                                                                                                                                 49290 MW; D6E987FA3D95BE30 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein ECU08_0540.
ECU08_0540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last annotation update)
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                                                                                                                                        EMBL; AF428334; AAL16264.1; -.. EMBL; AY074352; AAL67048.1; -.. EMBL; AC006072; AAM15133.1; -.. EMBL; AC006072; AAM15133.1; -..
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
00703811.5 protein.
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                                                                                                                                                                                                                        Hypothetical protein. SEQUENCE 442 AA; 4
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Best Local Similarity
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Liu S.X., Sakano H., Pham P.K., Yamada K., Banh J., Etgu P., Lee J.M.,
Liu S.X., Sakano H., Pham P.K., Davis R.W., Ecker J.R., Theologis A.;
Toriumi M., Yu G., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"Full Length cDNA of gene K8K14.2 (GI:9758429).";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned Pl clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                           Gaps
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Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
              Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Pernsier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Delbac F., El Alaoui H.; Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.; "Genome sequence and gene compaction of the eukaryote parasite Nature 414.450-453(2001).

BMBL; AL590448; CAD26359.1; -.
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative myb-related protein (Myb-related protein, 33.3K).
                                                                                                                                                                                                                                Score 35; DB 5; Length 291;
Pred. No. 39;
1; Mismatches 1; Indels
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-: SUBMICELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-: SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.

EMBL, AF326877; AAG41459.1;
                                                                                                                                                                                          291 AA; 31902 MW; 70ABBB450CD45D35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Full Length cDNA of gene K8K14.2 (GI:9758429).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HASE'S PLILOS, TECHNICAL BRAIN BONA BINDING.
INTERPECO, IPPRO1105, Myb. DNA-binding, 2.
PRO111, SM001395, SANT, 2.
PROSITE, PS00037; MYB.1; 1.
PROSITE; PS000334; MYB.2; UNKNOWN.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
MEDLINE=21576510; PubMed=11719806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB007645; BAB09015.1; -. AF339698; AAK00380.1; -.
                                                                                                                                                                                                                                72.9%;
75.0%;
                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 4:401-414(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P01103; 1POM.
                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 268 QMASEDPP 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                             1 QQSSEDPP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tabata S.;
                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9FDW1
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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Plana P.K., Quach H.L., Sakurai T.,
Satou M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
AT$607300/K8K14_2.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Agendiophyta; audicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Nguyen M., Onodera G.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yannada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
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0
                                                                             DB 10; Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.9%; Score 35; DB 10; Length 305; 85.7%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Arabidopsis cDNA clones."; Submitted (AUG-2001) to the {\tt EMBL/GenBank/DDBJ} databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ecker J.R.;
"Arabidopsis ORF clones ";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AYO52293; AAL31250.1; -..
EMBL; AYO61923; AAL31250.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR01005; Myb_DNA_binding.
Pfam; PF00249; myb_DNA_binding; 2.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
PROSITE; PS00034; MYB_2; UNKNOWN_2.
PROSITE; PS50090; MYB_3; 2.
SEQUENCE 305 AA; 33282 MW; FDD31F990BDDBE4F CRC64;
PROSITE; PS50090; MYB_3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 305 AA; 33268 MW; FDD31F9916E14D9D CRC64;
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0
                                                                                                                                                                                                                                                                                           305 AA.
                                                                                               Pred. No. 41;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                           72.9%; Score 35;
85.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q15523;
01-NOV-1996 (TrEMBLrel. 01, Created)
                                                       Query Match
Best Local Similarity 85./.
6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                             ||:||||
186 SSDDPPT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 SSDDPPT 192
                                                                                                                                                       3 SSEDPPT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     015523
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                                                                                                                                                                                                                                                                         Q941B3
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Query Match
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                                                                                                                         RESULT 12
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                                                                                                                                                                                                                                                                                                                                                    ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 479 AA; 53005 MW; 1ADFB5B548828485 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthazia; Rodentia; Sciurognathi; Muridae; Murinae, Mus.
                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                       Chu W., Presky D.H., Danho W., Swellick R.A., Burns D.K.;
Chu W., Presky D.H., Danho W., Swellick R.A., Burns D.K.;
Identification and characterization of DBK, a novel putative
serine/threonine protein kinase from human endothelial cells.";
Eur. J. Biochem. 225:695-702(1994).
Eur. J. Sinchant 225:695-702(1994).
EMBL; X80229; CAA56515.1;
HSSP; P05132; IATP.
                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                         72.9%; Score 35; DB 4; Length 479; 66.7%; Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF305088; AAK32110.1; -.
EMBL; BC004660; AAH04660.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SMUUUJJ; ____.
PROSITE; PS50021; CH; I.
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                             Interpro; IPR000719; Euk_pkinase.
Interpro; IPR000961; Pkinase_C.
Interpro; IPR000290; Ser_thr_pkinase.
Pfam; PF00069; pkinase_C: 1.
Pfam; PF00433; pkinase_C: 1.
Probom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00133; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00117; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tangerin B (Similar to KIAA0903 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; Q01082; 1BKR.
InterPro; IPR001715; Calponin-like.
InterPro; IPR001230; Prenyl_site.
                                                                                                  SEQUENCE FROM N.A.
MEDLINE=95045520; PubMed=7957185;
                         Serine/threonine protein kinase.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00307; CH; 1.
SMART; SM00033; CH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 QKSSRDPPS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QQSSEDPPT 9
                                                                         NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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RX STRAIN-EBKRELEY;
RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA dams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelifer B.D.,
RA Brandon R.C., Robert E.G., Helf G., Nelson C.R., Malklos G.L.G.,
RA Abril J.F., Agbayari A., A H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beesson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beesson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berty J.M., Cawley S., Dahlke C., Davenpoll L., Basaley E.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Durkov B.C., Dunn P.
RA Altris N.L., Derngelista C.C., Ferraz C., Ferraz C., Ferraz C., Ferraz C., Gabrieltan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Durbin K.J. Erangelista C.C., Ferraz C., Ferraz S., Pleatschman W.,
RA Harris N.L., Harvey D., Helman T.J., Herrandez J.R., Herris M.,
A Harris N.L., Mouston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
A John D., Houston K.A., Mowland T.J., Wei M.-H., Ibegwam C.,
A John D., Houston K.A., Mowland T.J., Wei M.-H., Ibegwam C.,
A Hostin D., Houston K.A., Moy M., Murphy B., Moshnefi A.,
A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshnefi A.,
A Reinert K., Remington K.A., Mixon K., Musskenn D.K., Pacieb J.M.,
RA Reinert K., Remington K.A., Mixon K., Pottler E., Wang K., Shand R.,
A Shreks R., Tector C., Turner R., Venter E., Wang K., Shand S., Pollard J., Wang S., Yao Q.A.,
RA Wallams S.M., Woodage T., Singson M., Strong R., Shand R., Shing S., Jahon M., Shong K., Jungson M., Strong K., Shen M., Shong K., Jungson M., Strong K., Shen M., Strong K., Shen M., Strong K., Shen M., Zhong X., Zhu S., Zhu S., Zhu S., Zhu S., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                   Gaps
                                                                               ó
   Score 35; DB 11; Length 874; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1068 AA; 118348 MW; 9E50BDCDD343995B CRC64;
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NAY-2000 (TrEMBLrel. 13, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CG14442 protein.
                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0029893; CG14442.
InterPro; IPR000425; MIP_family.
PROSITE; PS00221; MIP; UNKNOWN_1
72.9%;
85.7%;
       Query Match 72.99
Best Local Similarity 85.79
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00221; MIP; SEQUENCE 1068 AA; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                         :1|||||
327 TSEDPPT 333
                                                                                                                                                              3 SSEDPPT 9
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Length 1068;

DB 5;

72.9%; Score 35;

Fri Feb 14 15:01:00 2003

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9FG10
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
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                 0
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0
                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,

Goldsmith A.D., Lee J.M., Quach H.L., Toriuni M., Yu G., Bowser L.,

Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,

Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Trull Length cDNA of gene F15M7.13/AT5g06600 (GI:10178116).";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF5860198, AAK59081.; -.
R InterPro; IPR0012083; MATH.
R InterPro; IPR001448; SASP.
R InterPro; IPR001448; SASP.
R InterPro; IPR001448; OCH-2.
R Pfam; PF00240; ubiquitin.
R Pfam; PF00442; UCH-1.
R Pfam; PF00443; UCH-2.
R PROSITE; PS00304; SASP 1; UNKNOWN_1.
R PROSITE; PS00973; UCH_2.2; 1.
R PROSITE; PS00295; UCH_2.2; 1.
                           ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1115;
66.7%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 10; Length 11
Pred. No. 1.6e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1115 AA; 130478 MW; 4AB4E10D836C2172 CRC64;
                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative ubiquitin carboxyl-terminal hydrolase.
F15M7.13/AT5G06600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                         PRT; 1115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
Ubiquitin-specific protease 12.
UBP12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.9%;
75.0%;
                         6; Conservative
                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
           Best Local Similarity
                                                                        114 QQQSQQPPT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ery Match
st Local Similarity
                                                1 QQSSEDPPT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :|||||
46 QPAEDPPT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 QSSEDPPT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                     Q9C5K1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09FPT1;
                                                                                                                                       Q9C5K1
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                         Matches
                                                                                                               RESULT 13
Q9C5K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
09FPT1
10 09FPT
AC 09FPT
DT 01-MA
DT 01-MA
DT 01-JU
DE Ubiqu
GN UBP12
OC EUKAR
OC SPERM
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RRA
RRA
RRA
RRA
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RA
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SQ
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MEDLINE-20567829; PubMed-11115897;

MEDLINE-20567829; PubMed-11115897;

MEDLINE-20567829; PubMed-11115897;

Yan 'N. Docalling J'H., Fablel T'G., Durski A.M., Vierstra R.D.;

Are Required for the Resistance to the Amino Acid Analog Canavanine.";

RE Plant Physiol. 124:1828-1843(2000).

RE MBL; AF302663; AA42754-1;

RE MBL; AF302663; AA42754-1;

REPTO: IPR000148; SASP.

RICEPTO: IPR001448; SASP.

RICEPTO: IPR0001594; UCH-2.

REPTO: IPR001594; UCH-2.

REPTO: IPR00140; Uniquitin, 1.

REPTO: IPR00439; UCH-2.

REPTO: IPR0143; UCH-2.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Ublquitin carboxyl-terminal hydrolase.
Arabidopsis thallana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Arassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Target as:

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AP00243; BARIL409.1; -.

InterPro; IPR001448; SASP.

InterPro; IPR001448; SASP.

InterPro; IPR001448; SASP.

InterPro; IPR00147; UCH-2.

R InterPro; IPR00147; UCH-2.

R Pfam; PF00442; UCH-2.

R Pfam; PF00443; UCH-2.

R PROSITE; PS00037; UCH-2.1.

R PROSITE; PS00972; UCH-2.1.

R PROSITE; PS00973; UCH-2.2; 1.

R PROSITE; PS00973; UCH-2.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
Tabata S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.9%; Score 35; DB 10; Length 11
75.0%; Pred. No. 1.6e+02;
Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1116 AA; 130640 MW; E5534164E5B66C88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1126 AA; 131869 MW; 2478F44417BF1768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1126 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00304; SASP_1; UNKNOWN_1.
PROSITE; PS00972; UCH_2_1; 1.
PROSITE; PS00973; UCH_2_2; 1.
PROSITE; PS50235; UCH_2_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 75.0 tes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 OPAEDPPT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eurosids II; Bra:
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 QSSEDPPT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protease.
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Gaps

2 QSSEDPPT 9 | :||||| | 56 QPAEDPPT 63 δy

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Search completed: February 14, 2003, 11:18:45 Job time : 20.8925 secs

